boun toming

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OM protein – protein search, using sw model

January 17, 2001, 13:36:41; Search time 25.93 Seconds (without alignments) 21.099 Million cell updates/sec Run on:

US-08-765-837-5 86 Title: Perfect score: Sequence:

1 ENOROGAEPRKNEVKP 16

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

268485 seqs, 34193795 residues Searched:

112136 Total number of hits satisfying chosen parameters:

length: 0 length: 16 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

/SIDSI/goddata/geneseqp/AA1992.DAT:*
/SIDSI/goddata/geneseqp/AA1992.DAT:*
/SIDSI/goddata/geneseqf/geneseqp/AA1993.DAT:*
/SIDSI/goddata/geneseqf/geneseqp/AA1995.DAT:*
/SIDSI/goddata/geneseqf/geneseqp/AA1995.DAT:*
/SIDSI/goddata/geneseqf/geneseqp/AA1995.DAT:*
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/SIDSI/goddata/geneseqf/geneseqp/AA1999.DAT:* A_Geneseq_36:*

| SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d				
Result		Query				
No.	Score	Match	Watch Length DB	DB	ID	Description
1	09	69.8	15	8.7	W08420	A Principal At A Principal
7	36	41.9	16	18	W08419	Factor IX binding
3	33	38.4	15	18	W08421	Factor IX binding
4	30	34.9	80	19	W75817	Mouse mast coll
ស	30	34.9	14	16	R83129	Himan GMDC truth
9	28	32.6	80	16	R66094	Myelonojetjo proge
7	28	32.6	12	18	W34873	Himan tau proteio
8	28	32.6	13	20	Y42676	HHV-6 variant A do
0	28	32.6	14	16	R66092	Myelopoietic proce
10	28	32.6	14	19	Y20167	Himan P53 imminode
11	28	32.6	14	19	W81782	Himan LEA pritono
12	28	32.6	15	12	R12025	N-terminal of prot

Framework 2 region	Antiqen peptide fr	CD44 epitope. Rat	1	Tyrosine phosphata	Mouse Ind2A upper	Immunogenic popti		KAGE DO	Peptide 23 derived	TNF receptor bind	Fragment of G. oxy	hina	Growth hormone re	Sequence of Tag2A	-	_	Buman growth hormo	C-terminal binge		IgG2A mouse antige	•	N-terminal sequence	Growth hormone re	StearoylACP-desa	Peptide (79) inhib	(222)	(151)	i hody r		. 60	
W79210	R95642	W01827	R55685	Y59337	W99342	Y46552	W44211	W33765	Y91911	R91945	W69499	R55176	R10061	R37640	Y16424	X13338	W93125	W88090	Y98918	Y57245	Y80915	R20012	R31436	R82023	R57579	R57722	R57651	R03909	Y88537	R21059	
19	17	18	15	21	20	20	18	18	21	17	19	15	12	14	17	20	20	20	21	21	21	13	14	16	15	15	15	11	21	13	
15	13	14	15	16	6	10	11	11	12	13	13	14	15	15	15	15	15	15	15	15	15	16	16	16	σ	σ	σ	10	11	13	•
32.6	31.4	31.4	31.4	31.4	30.2	30.2	30.2	30.2	30.2	٠:		30.5		30.2		30.2		30.2		30.2		-	30.2	30.2	29.1	29.1	29.1	29.1	29.1	29.1	
58	27	27	27	27	26	56	56	56	56	56	56	56	56	56	56	26	56	56	56	56	56	26	56	56	25	22	25	52	52	25	
13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	•

ALIGNMEN'S

RESULT W08420

W08420 standard; peptide; 15

¥

W08420;

(first entry) 04-SEP-1997

Factor IX binding peptide #4 from factor VIII A3 domain exosite I.

Exosite; factor VIII; A3 domain; activated factor IX; precursor; thrombotic disorder; inhibition; intrinsic blood coagulation pathway.

Homo sapiens

WO9641816-A1

27-DEC-1996.

96WO-NL00236. L2-JUN-1996;

95EP-0201554 12-JUN-1995; (BLOE-) STICHTING CENT LAB VAN DE BLOEDTRANSFUSI.

Lenting PJ, Mertens K;

WPI; 1997-065422/06.

Factor VIII peptide that binds to factor $\ensuremath{\text{IX}}$ - useful for treating thrombotic disorders

Example 2; Page 17; 39pp; English.

The sequences given in W08417-24 represent peptides derived from

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RESULT
                                     W08421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in W08417-24 represent peptides derived from exosite I derived from factor VIII A3 domain. The exosite regions have low hydropathy values which reflects their hydrophilic nature. These peptides and fragments derived from them are cappable of binding-activated factor IX and its non-activated precursor. These peptides can be used for treating thrombootic disorders by inhibiting the intrinsic blood coagulation pathway. This peptide corresponds to Factor VIII A3 domain region 1786-1801.
exosite I derived from factor VIII A3 domain. The exosite regions have low hydropathy values which reflects their hydrophilic nature. These peptides and fragments derived from them are capable of binding-activated factor IX and its non-activated precursor. These peptides can be used for treating thrombotic disorders by inhibiting the intrinsic blood coagulation pathway. This peptide corresponds to Factor VIII A3 domain region 1799-1813.
                                                                                                                                                                                                                                                                                                                                                   Exosite; factor VIII; A3 domain; activated factor IX; precursor; thrombotic disorder; inhibition; intrinsic blood coagulation pathway
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor IX - useful for treating
                                                                                                                                                                                                                                                                                                                              Factor IX binding peptide #3 from factor VIII A3 domain exosite
                                                                                                                                                       ;
0
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                                                                                                                                 Length 15;
                                                                                                                                                       Indels
                                                                                                                                DB 18; L
0.00024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BLOE-) STICHTING CENT LAB VAN DE BLOEDTRANSFUSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1
Pred. No. 4.6;
1; Mismatches
                                                                                                                                                       Mismatches
                                                                                                                                Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Factor VIII peptide that binds to thrombotic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 17; 39pp; English.
                                                                                                                                                                                                                                                           W08419 standard; peptide; 16 AA.
                                                                                                                                69.8%; Scallarity 100.0%; P: Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-0201554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-065422/06.
                                                                                                                                                                              6 GAEPRKNFVKP 16
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                               15 AA
                                                                                                                                                                                                                                                                                                                                                                                                             WO9641816-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-1995;
                                                                                                                                                                                                                                                                                                         04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lenting PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                Sequence
                                                                                                                                                                                                                                                                                  W08419;
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                                                                                                                                                                                                                                      RESULT
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Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma; tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria; antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis, hyperproliferative skin disease; peptic ulcer; hyperresponsiveness; inflammatory skin condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in W08417-24 represent peptides derived from exosite I derived from factor VIII A3 domain The exosite regions have low hydropathy values which reflects their hydrophilic nature. These peptides and fragments derived from them are capable of binding-activated factor IX and its non-activated precursor. These peptides can be used for treating thrombotic disorders by inhibiting the intrinsic blood coagulation pathway. This peptide corresponds to Factor VIII A3 domain region 1804-1818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                     Exosite; factor VIII; A3 domain; activated factor IX; precursor; thrombotic disorder; inhibition; intrinsic blood coagulation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Factor VIII peptide that binds to factor IX - useful for treating
                                                                                                                                          Factor IX binding peptide #5 from factor VIII A3 domain exosite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18; Length 15;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse mast cell protease (mMCP-6) susceptible peptide 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BLOE-) STICHTING CENT LAB VAN DE BLOEDTRANSFUSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 15;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 17; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.4%; SCU-
100.0%; Pre
0;
W08421 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W75817 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lenting PJ, Mertens K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombotic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-065422/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 KNFVKP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-0CT-1998
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| knfvkp
                                                                                                                                                                                                                                                                                                          WO9641816-A1
                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1995;
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        27-DEC-1996.
                                                                                              04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W75817;
                                                  W08421;
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Gaps

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Indels

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1 ENQROGAE 8

δ g

WO9833812-A1

Synthetic.

Wus sp

06-AUG-1998

05-FEB-1997; 30-JAN-1998;

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New isolated human guanosine 5'-mono.phosphate synthetase - used to develop prods. for its study and for identifying inhibitors useful for
                                                                                                                                                    digested with trypsin. When tryptic peptides were resolved. Their sequences are given in R83124-R83132 and are indicated on R83122 FF. Based on the peptide sequences, degenerate oligos were synthesised in both the sense and antisense orientations and used in PCR. A fragment was generated with oligos 252 and 8A2 (see T00493 FF). 252 & 8A2 corresp. to tryptic peptides 2 & 8. This PCR fragment (pcr. 258A) (see T00493 FF) was used to screen an A3.01 cDNA library. The complete sequence of positive clone 6 (GMPS.6 T00492) was determined and is shown in Figure 1 (T00493). The derived AA sequence (R83123) of human GMP synthetase is shown in Figure 1 (R83122). The predicted mol. wt. of the enzyme - 76,725 - was in good agreement with the size indicated by polyacrylamide gel electrophoresis of the purified A3.01 human GMPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides are claimed which contain at least 5 (pref. 5-20) amino acids and which include the sequence Ala-Lys-Pro-Arg. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for
                                                                                                                                     Naturally occurring human GMPS was purified from A3.01 cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .:
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myelopoletic; myeloid; progenitor cell inhibitor; leukaemia; polycythemia; myelosuppression; septic shock; hypotension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide(s) that suppress myeloid progenitor cell proliferation - contain the sequence Ala Lys Pro Arg, us treating or preventing e.g. leukaemia, radiation induced myelosuppression and septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cooper S, Kreisberg M, Kreisberg R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myelopoietic progenitor cell inhibitor peptide.
                                     develop prods. for its study and for identify e.g. anti-cancer or immunosuppressive therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                  Example; Table 2, page 18; 48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 40; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R66094 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US05773.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AA;
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3 eplkdfik 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R66094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lu L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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QQ
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences shown in W75807 to W75835 represent mouse mast cell protease (mMCD-6) susceptible peptides obtained in the absence of heparin. The invention provides sequences shown in W63160 to W63160 that are finhibitors of mMCP-6. These tryptase-6 complex inhibitor peptides can be used for treating a mast cell-mediated inflammatory disorder. The inhibitors can be used to treat inflammatory disorders including asthma, allergic rhinitis, urticaria and antioedema, eczematous dermatitis (atopic dermatitis), hyperproliferative skin disease, anaphylaxis, pepticuloges, inflammatory bowel disorder, hyperresponsiveness and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                       Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated inflammatory disorders e.g. asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 19; Length 8; Pred. No. 2.1e+05; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human guanosine 5'-monophosphate synthetase; A3.01 cells; tryptic peptide.
                                                                                                                                                                                                                (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Page 26; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R83129 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GMPS tryptic peptide # 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.9%;
62.5%;
                                                                                                                                                                         97US-0037090
                                                                                                                                   98WO-US01865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYNT ) SYNTEX USA INC.
                                                                                                                                                                                                                                                        Huang C, Stevens RL;
                                                                                                                                                                                                                                                                                                WPI; 1998-437390/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barnett JW, Lou L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-366393/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skin conditions.
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Sequence

Query Match

ò QQ 07-APR-1995; 08-APR-1994;

WO9527789-A 19-0CT-1995.

Synthetic.

R83129;

RESULT R83129

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Caps

888888888

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The first control that comprises contacting host cells with immunological reagents specific for an epitope of HHV-6 variant A and/or B major immediate early protein (MIEP). HHV-6 peptides for raising an immunological reagent that binds specifically to an epitope of: (a) HHV-6 variant A and not B MIEP; or (b) HHV-6 variant A and B MIEP are also provided. The peptides are useful as immunological, reagents, e.g. hyperimmune sera. Monoclonal antibodies and recombinant DNA-derived single chain fragment variables (SCFV) may be useful for detecting HHV-6 infection when raised against specific epitopes of the HHV-6 of sensitivity and specificity. The methods also have shortened turns around time (compared to other known methods, e.g. the isolation of the virus in cell culture, the detection of virus DNA in an acellular specimen by PCR or positive immunohistochemical staining) and can be easily implemented by a diagnostic laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sthods for the rapid detection of human herpes virus 6 variants A and utilizing antibodies raised against synthetic peptides \,
                                                                                                                                         Human herpes virus-6; HHV-6; infection; immunological; MIEP; epitope; major immediate early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for detecting human herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 20; Length 13;
Pred. No. 96;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myelopoietic progenitor cell inhibitor peptide.
                                                                                                         HHV-6 variant A derived peptide epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 42; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R66092 standard; peptide; 14 AA.
   Y42676 standard; peptide; 13 AA.
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41.78;
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                                                                                                                                                                                                                                                                                                                           99WO-US06921
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Best Local Similarity 41./*,
Sinconservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-1995 (first entry)
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kehl KK;
                                                                                                                                                                                                                                                                                                                                                                                                                 (CARR/) CARRIGAN D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ENQROGAEPRKN 12
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                                                                                                                                                                                                                   Human herpesvirus 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-601224/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (KEHL/) KEHL K K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carrigan DR,
                                                                      17-JAN-2000
                                                                                                                                                                                                                                                                                                                          26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                             26-MAR-1998;
23-MAR-1999;
                                                                                                                                                                                                                                                   W09949086-A1
                                                                                                                                                                                                                                                                                      30-SEP-1999.
                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methods
                                     Y42676;
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                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide containing part of
for detecting Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An antibody, prepared using a partial peptide containing the phosphorylated residue of the phosphorylated tau protein, e.g. the present sequence, in a paired helical filament, can be used to detect Alzheimer's disease, i.e. by detecting phosphorylated tau protein in brain extracts or tissue fragments.
              The peptides suppress proliferation of myeloid progenitor cells and reduce susceptibility to septic shock. They are used to treat chronic myelogenous leukaemia or polycythemia, to reduce chemotherapy or radiation-induced myelosuppression, to prevent septic shock and to reduce nitric oxide-induced hypotension.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; phosphorylated tau protein; paired helical filament; detection; Alzheimer's disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 18; Length 12;
Pred. No. 89;
1; Mismatches 1; Indels
                                                                                                                                                                            Length 8;
                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uchida
 claimed such peptide.
                                                                                                                                                                            Score 28; DB 16;
Pred. No. 2.1e+05;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody prepared using a partial phosphorylated tau protein - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 36; 48pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                          W34873 standard; peptide; 12 AA.
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32.6%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                            Query Match 32.6%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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sequence is a specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tau protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-470978/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AA;
                                                                                                                          AA;
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1 akpranf 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example;
                                                                                                                            Sequence
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RESULT W34873

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RESULT Y42676

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WO9845322-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzhelmer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M; neurofilament-F; presenilin II; presenilin II; cellular tumour antigen; glial fibrillary acidic protein; GFAPP; p53; semaphorin III; HUPF-I; bcl-2; B-cell leukemia/lymphona 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides are claimed which contain at least 5 (pref. 5-20) ami acids and which include the sequence Ala-Lys-Pro-Arg. The present sequence is a specifically claimed such peptide.

The peptides suppress proliferation of myeloid progenitor cells and reduce susceptibility to septic shock. They are used to treat chronic myelogenous leukaemia or polycythemia, to reduce chemotherapy or radiation induced myelosuppression, to prevent septic shock and to reduce nitric oxide-induced hypotension.

The present sequence is the preferred peptide for clinical use.
                                                                                                                                                                                                                                                                                                                                                                            New peptide(s) that suppress myeloid progenitor cell proliferation - contain the sequence Ala Lys Pro Arg, useful for treating or preventing e.g. leukaemia, radiation induced myelosuppression and septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
             Myelopoietic; myeloid; progenitor cell inhibitor; leukaemia; polycythemia; myelosuppression; septic shock; hypotension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 16; Length 14;
Pred. No. 1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                     Kreisberg M, Kreisberg R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human P53 immunogenic peptide fragment.
                                                                                                                                                                                                                                               (RESE ) RESEARCH CORP TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y20167 standard; Peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.6%;
71.4%;
                                                                                                                                                                           94WO-US05773.
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                                                                                                                                                                                                                                                                                     Cooper S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                        WPI; 1995-022707/03.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AA;
                                                                                                                                                                                                                                                                                                    Moore RN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AEPRKNF 13
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                                                                                                                                                                                                                                                                                     Broxmeyer HE,
                                                                                                                                                                         18-MAY-1994;
                                                                                                                                                                                                             20-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                   WO9428013-A
                                                                                                                                       08-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenic
                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y20167;
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This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, and littles typer II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may but caused by mutations in RNA rather than bNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated protein 2 (MAP2), neurofilament-1, neurofilament-1, neurofilament-1, neurofilament-1, neurofilament-1, neurofilament-1, neurofilament-1, neurofilament-1, presenilin II; presenilin II; HUPF-1, high mobility group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations – used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HE4; epididymis-specific; diagnosis; male infertillity; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-C (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                Leeuwen FW;
                                                                                                                                                                                                               ROYAL NETHERLANDS ACAD ARTS & SCI.
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                                                                                                                                                                                                                                                  UNIV ROTTERDAM ERASMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.6%;
62.5%;
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                                                             98WO-IB00705
                                                                                                                    97US-0043163
                                                                                                                                                                                                                                                                                                            Burbach JPH, Grosveld FG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                     (UYUT-) RIJKSUNIV UTRECHT.
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Best Local Similarity
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                                                             02-APR-1998;
                                                                                                                       LO-APR-1997;
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15-0CT-1998
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                                                                                                                                                                                                                     ROYA-)
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W81782
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This represents the amino acid sequence of the framework 2 region of human V kappa gene HUM5400. This is used to consruct a humanised anribody LO-CD2a. The invention relates to the use of the monoclonal antibody (MAD) LO-CD2a or a humanised or a chimeric version of the LO-CD2a antibody for the inhibition of a T-cell mediated immune response in a patient. The MAD LO-CD2a (produced by hybridoma cell line ATC HB 11423) can bind to an epitope on the CD2 antigen of the human lymphocytes. The T-cell mediated immune response in a patient can be inhibited by administering the MAD LO-CD2a or an antibody that binds to the same human lymphocyte epitope as LO-CD2a. The method is used for preventing transplant rejection or for treating graft-versus-host disease or for treating autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; MAb; LO-CD2a; humanised antibody; CD2 antigen; human lymphocyte; immune response; chimeric; graft-versus-host disease; T-cell; transplant rejection; autoimmune disease; HUM5400.
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibition of T-cell mediated immune response with anti-CD2 monoclonal antibody LO-CD2a - used for preventing transplant rejection or for treating graft-versus-host disease or auto-immune diseases
                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 19; Length 15;
Pred. No. 1.1e+02;
1; Mismatches 3; Indels
                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Framework 2 region of human V kappa gene HUM5400
                                                                           Score 28; DB 12;
Pred. No. 1.1e+02;
                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Columns 33-34; 96pp; English.
                                                                                                                                                                                                                                                                                   W79210 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYLO-) UNIV CATHOLIQUE LOUVAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0027008.
93US-0119032.
95US-0407009.
                                                                         32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.6%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0472281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0472281
                                                                                                                                                                                                                                                                                                                                                            21-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-556337/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bazin H, Latinne D;
                                                                                                                                                     1 ENQRQGAEPRK 11
                                                                                                                                                                                         3 edgedgydprk 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                              Best Local Similarity
                         AA;
                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1993;
09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5817311-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-1998.
                       Sequence
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                              RESULT 13
W79210
                                                                                                                  Matches
                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel human epididymis-specific protein, HE4 epitope fragment. This protein may be used for Cloning and for expression of human epididymis specific polypeptides in prokaryotic or eukaryotic host cells. Such proteins and antibodies generated from them may be used for diagnosis of e.g. male infertility. The polypeptides and antibodies may also be used for treatment of male infertility and for immunosterilisation of mammans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein having human protein C and activated human protein C activity - has natural human protein structure with aminoacid from 12th to terminal position e.g. aspartic acid.
                                                                                                                                                                                                                                              DNA encoding human epididymis polypeptides – useful for, e.g. diagnosis of male infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 14; 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is one of several new N-terminals for human protein C. See also R12022-R12031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB
Pred. No. 1e+0.
4; Mismatches
                                                                                                                               (IHFH-) IHF INST HORMON & FORTPFLANZUNGS.
                                                                                                                                                                                                                                                                                                    Example 9; Page 19; 29pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal of protein C analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clalm 1; Page 1; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R12025 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.68;
                                                                                           90DE-4002981.
                                                                         90DE-4038189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89JP-0229539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89JP-0229539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                      Kirchhoff C;
                                                                                                                                                                                                           WPI; 1998-585748/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NOROGAEPRKN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-276411/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ndkegsapgvn 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TEIJ ) TEIJIN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q11737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP03091479-A
                                      29-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1989;
                                                                                            01-FEB-1990;
18-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                  Ivell R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R12025;
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T cells expressing fusion protein specific for variant CD44 gene useful for cancer therapy, esp. pancreatic carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The fusion protein (T62573) comprises a first portion having
                                                                                                                                                                                            T-cell; receptor; CD44; epitope; fusion protein; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
(GESL ) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
                     W01827 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 9; 16pp; English.
                                                                                                      20-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-101136/10.
                                                                                                                                                                                                                immunoglobulin.
                                                                                                                                                                                                                                                         Rattus rattus.
                                                                                                                                                                                                                                                                                                   DE19540515-C1
                                                                                                                                                CD44 epitope
                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-1995;
                                                                                                                                                                                                                                                                                                                                          06-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hekele A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
    W01827
                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This peptide antigen is derived from the mature C-terminal domain of human articular cartilage-derived morphogenetic protein-1 (CDMP-1, R95635), and has been used to generate polyclonal antibodies in rabbits. The peptide does not show sequence identity with any other known protein, including bone morphogenetic protein. The resulting antibodies have been used to screen tissues from human embryos, to study differential CDMP gene expression. At 6 wk, CDMP-1 is detected in precartilage condensations, and at 7.5-8.5 wk CDMP-1 is found in cartilaginous cores of long bones. In areas of active cartilage degradation and bone matrix formation, CDMP-1 expression is also detected in hypertrophic chondrocytes. No expression is detected in the axial skeleton, and only low levels are present in other tissues. CDMP-1 is present in a purified cartilage extract (claimed) which stimulates local cartilage of commation and repair when combined with a matrix and implanted in a mammal. The protein may be used in therapy of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or to repair cartilage effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified cartilage extracts and proteins - used to stimulate the development and repair of cartilage in vivo.
                                                                                                                                                                                                                                                                                                                  Human, antigen: cartilage-derived morphogenetic protein-1; CDMP-1; polyclonal antibody: rabbit; articular cartilage; chondrogenic; vulnerary; implantation; chondromalacia; osteoarthritis; therapy;
                                                                                                                                                                                                                                                                           Antigen peptide from cartilage-derived morphogenetic protein-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 17; Length 13; Pred. No. 1.4e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 15; 34pp; English.
                                                                                                                                              R95642 standard; Peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moos M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.4%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US12814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US12814
                                                                                                                                                                                                                                   26-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luyten FP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-251714/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
3 QRQGAEPRK 11
                                       4 grpggsprr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                  joint repair
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9614335-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang
                                                                                                      14
                                                                                                      RESULT
                                                                                                                            R95642
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Ponta H;

Herrlich P,

95DE-1040515.

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0
specific affinity for an amino acid sequence encoded by a variant exon of the CD44 gene (pref. W01827 Itat) or W01828 [human]), and a second portion comprising at least part of the amino acid sequence of a subunit of the T-cell receptor complex or of an immunoglobulin receptor. Products contg. the fusion protein (or DNA encoding it) are useful for treating cancer, esp. mammary, colonic, gastric or pancreatic carcinoma, and metastatic disease.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                    Length 14;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                  Score 27; DB 18; L. Pred. No. 1.6e+02; 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 17, 2001, 13:36:43 Job time: 118 sec
                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                    31.4%; 55.6%;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             14 AA;
                                                                                                                                                                                                                                                                                                                                                                 1 ENQROGAEP 9
                                                                                                                                                                                                 Sequence
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.; 0

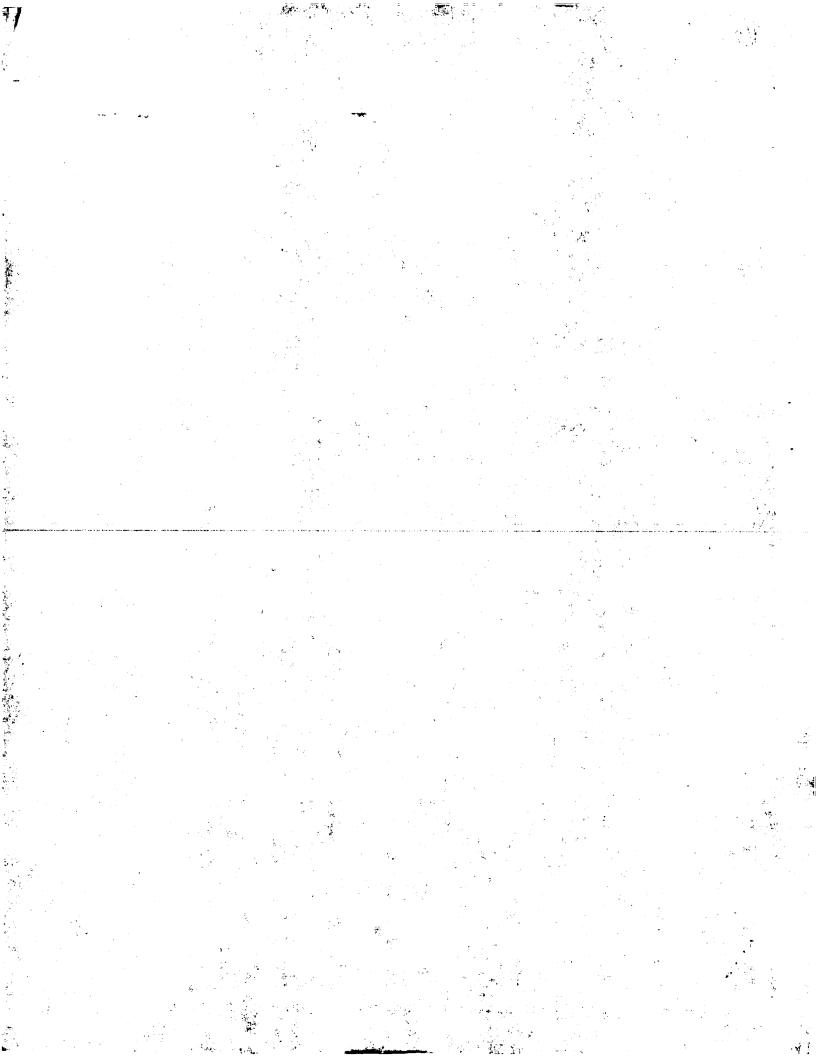
Gaps

ö

5; Conservative

5 QGAEPRKN 12 ıı i il 1 qgkrpskn 8

ò g RESULT



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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

January 17, 2001, 13:38:36 ; Search time 20.45 Seconds (without alignments) 53.125 Million cell updates/sec

US-08-765-837-5 86 1 ENQRQGAEPRKNFVKP 16 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 segs, 67900655 residues Searched:

2778 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical MN1/T	bradykinin-potenti	placental calcium-	protein QA100044 -	apolipoprotein Cb2	acidic fibroblast	alpha-conotoxin Ep	bradykinin-potenti	celF protein - Esc	hypothetical prote	NADH dehydrogenase	acetylcholinestera	translation elonga	pollen major aller	angiotensin-conver	bradykinin-potenti	R-phycoerythrin ga	potassium channel	scotophobin - rat	28K serine protein	D-galactose-bindin	ribosomal protein	ribosomal protein	calliFMRFamide 1 -	calliFMRFamide 10	calliFMRFamide 4 -	locustamyotropin -	histone H2B - huma	urinary tract ston
SUMMARIES	QI	138032	D37196	I49407	PA0046	S67975	803955	A59042	XASNBA	S42587	C40944	PQ0777	S68637	PD0441	A53252	XAVI9B	A37196	G22565	PS0443	SFRT	A35417	S29174	A28144	S35538	A41978	A44787	D41978	A43975	S65409	B56049
	DB	4	~	7	7	7	~	7	-1	7	7	~	7	7	7	~	7	7	7	, -	7	7	7	7	N	7	7	Н	7	7
	Query Match Length	15	11	15	15	15	15	16	11	11	14	7	11	11	12	13	13	13	13	15	15	15	16	σ	6	6	6	12	12	12
dР	Query	27.9	25.6	25.6	25.6	25.6	25.6	25.6	24.4	24.4	24.4	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23,3	23.3	22.1	22.1	22.1	22.1	22.1	22.1	22.1
	Score	24	22	22	22	22	22	22	21	21	21	20	20	20	20	20	20	20	20	20	20	20	20	19	19	19	19	19	19	19
	Result No.	1	7	ю	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

neurotensin - bovi	probursin tetradec	Ig heavy chain CRD	T-cell receptor al	alpha-2-macroglobu	physalaemin - trog	beta-glucosidase (callimiRFamide 1 -	ribosomal protein	protein 1.7 - commo	ovostatín - duck (leukotriene B-4 12	tubulin beta-3 cha	T-cell receptor be	T-cell receptor be	interphotoreceptor
UNBO	JH0328	PT0254	G41299	S33844	S07201	PQ0231	E44787	S36887	B44957	S00150	A47421	A39703	PH0762	S51735	G24417
П	ď	N	ď	~	a	~	~	7	~	7	~	7	7	~	7
13	14	14	15	10	11	11	12	13	13	14	14	14	14	15	15
-	_	. 1	'n.	6.	σ.	٥.	6.	6.	6.0	6.0	6.	<u>.</u> ق	6.0	20.9	6.0
22.	22.1	22	21	20	20	20	×	×	~	ñ	2	20	ñ	Ñ	Ñ
19 22.	19 22.	19 22	18.5 21	18 20	18 20	18 20	18 20	18 20	18 20				18 2(18 2

ALIGNMENTS

nt fusion nan) ence_revi an Baal, 995 2;22) (pl 1; MUID:9 GB/EMBL, is the ch 13 n 13 n tive 3;	human (fragment)	#text_change 20-Apr-2000	.; van der Plas, D.; Van Ke	oliferative disorders resul				CAA59398.1; PID:9971468 a translocation mutation.			•	Length 15; ; · Todals 0: imps 0:		
ltcal MN1/TEL mutant; ltcal MN1/TEL mutant; ltcb-1997 #sequence lt	fusion protein type I -	-revision 21-Feb-1997	3aal, S.; van Bezouw, S	2) (p13;q11) in myeloprown (p13;q11)		/ EMBL/ DUBJ		025; NID:g971467; PIDN:	•			46 46 C) ()		
TO T	 tical MN1/TEL mutant es: Homo sapiens (man)	21-Feb-1997 #sequence sion: 138032	, A.; Sherr, S.; van I e 10. 1511-1519, 1995	: Translocation (12,2)	A; Accession: I38032	s: Lransiated from ub, ule type: mRNA	ues: 1-15 <bui></bui>	<pre>-references: EMBL:X85(nt: This sequence is t</pre>	C;Genetics:	A; Gene: MN1/ETV6; MN1/TEL	A;Map position: 22q11/12p13 C;Keywords: fusion protein	Query Match 27 Best Local Similarity 37 Matches 3. Conservative	NOR	 4 NSKEGLOP 11

RESULT 2
bradykinin-potentiating peptide 4 - island jararaca
bradykinin-potentiating peptide 4 - island jararaca
C; Species: Bothrops insularis (island jararaca)
C; Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1', 1
C; Accession: B7196
R; Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentialing peptide
A;Reference number: A37196; MUID:90351557
A;Accession: D37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CIN>
C;Keywords: proglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

0 Gaps ö Query Match 25.6%; Score 22; DB 2; Length 11; Best Local Similarity 66.7%; Pred. No. 1.1e+03; Matches 4; Conservative 0; Mismatches 2; Indels

us-08-765-837-5.closed.rpr

: :

Gaps

; 0

Indels

Length 15;

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CKEYWORDS: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu F;1-16/Product: alpha-conotoxin Ep1 #status experimental <MAT>
F;2-8,3-16/Disulfide bonds: #status experimental
F;2-8,3-16/Binding site: sulfate (Tyr) (covalen!) #status experimental
F;16/Modified site: amidated carboxyl end (Cys) #status experimental
                                                                                                                                                                                                                                                                       N.Alternate names: alpha-endothalial cell growth factor
C;Species: Canis lupus familiaris (ddg)
C;Species: Canis lupus familiaris (ddg)
C;Bate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C;Accession: 803955
R;Quinkler, W.; Masaberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Sch Eur. J. Biochem. 181, 67-73, 1989
A;Title: Isolation of heparin-binding growth factors from bovine, porcine and canine A;Reference number: 803953; MUID:89231704
A;Accession: 803955
A;Molecule type: protein
A;Residues: 1-15 <QUI>C;Keywords: growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RiLoughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, J. B. alol. Chem. 273, 1567-1574, 1998
J. Blol. Chem. 273, 1567-1574, 1998
A.; Reference number: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that se A; Reference number: A59042; MUID:98288307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Conus episcopatus (bishop's cone)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
C;Accession: A59042
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bradykinin-potentiating peptide B - mamushi
C;Species: Agkistrodon blomhoffi (mamushi)
C;Species: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 2; Ler
Pred. No. 1.5e+03;
                             DB 2; Le
1.5e+03;
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                                                                               Mismatches
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                             Score 22;
Pred. No.
          25.6%; Scor.
100.0%; Pre
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60.0%;
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40.0%;
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A;Molecule type: protein
A;Residues: 1-16 <LOU>
C;Superfamily: alpha-conotoxin
                             Query Match 25.6
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 4; Conserv
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NYMKP 5
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7 GAEP 10
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                                                                                                                                                                       placental calcium-binding protein - western wild mouse (fragment)
(Species: Mus spretus (western wild mouse)
(Spacies: Mus spretus (western wild mouse)
(Spate: O.2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
(SAccession: 144407
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: 148934; MUID:94319082
A;Accession: 149407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Arabidopsis thaliana (mouse-ear cress).
C; Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C; Accession: PA0046; PA0042
R; Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
Submitted to JTPD, July 1994
A; Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A; Reference number: PA0001
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Blochem. 234, 586-591, 1995
A;Title: Characterization of apolipoproteins B-100, AI and C from plasma lipoprotein in A;Reference number: S67972; MUID:96128192
A;Accession: S67975
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C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S67975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross references: EMBL:U05696; NID:9497016; PIDN:AAA61936.1; PID:9497017
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.5e+03;
2; Mismatches 2;
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    goose (fragment)

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50.0%;
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A; Residues: 1-15 <KAM>
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A;Molecule type: protein
A;Residues: 1-15 <HER>
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-15 <RES>
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| AESKKGFL 8
QGAEPR 10
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QGGPPR 6
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EPRK 14
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C; Accession: A01254

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NAUR dehydrogenase (EC 1.6.99.3) 49K chain - fava bean mitochondrion (frayment)
N.Alternate names: complex I 49K chain; NADH--ubiquinone reductase 49K chain
C;Species: mitochondrion Vicia faba (fava bean)
C;Date: 03-May-1994 #sequence_revision 07-0ct-1994 #text_change 17-Mar-1999
C;Accession: P00777
R;Leternae, S: Boutry, M.
Plant Physiol: 102, 435-443, 1993
A;Title: Purification and preliminary characterization of mitochondrial camplex I (NA A;Refence number: P00775; MUID:94151437
A;Accession: P00775; MUID:94151437
A;Accession: P00775; MUID:94151437
A;Molecule type: protein
A;Residues: 1-7 <LETP
C;Comment: Complex I, mitochondrial NADH-ubiquiquinone reductase, is the first of the ranging from 5K to 75K.
C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone C;Genetics:
A;Genome: mitochondrion
C;Keywords: electron transfer; mitochondrion; oxidoreductase
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C;Species: Bos primigenius taurus (cattle)
C;Acces: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jun-1998
C;Accession: 568637
R;Boschetti, N.; Brodbeck, U.
FEBS Lett. 380, 133-136, 1996
A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of a si A;Reference number: 568637; MUID:96181683
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C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998
C;Accession: pD0441
C;Accession: pD0441
C;Accession: T: Uchida, T:; Sakal, T:; Kamo, M:; Morlmasa, T:; Tsugita, A. submitted to JIPID, August 1998
A;Description: Proteome analysis of mouse brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: brain
C; Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein
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Pred. No. 2.4e+03;
2; Mismatches 2;
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50.0%;
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Best Local Similarity 50.09
Matches 4; Conservative
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A; Residues: 1-11 <BOS>
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Best Local Similarity
Matches 4; Conserv
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2 RQGA 5
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: 542587
R;Guzzo, A.; DuBow, M.S.
Mol. Gen. Genet. 242, 455-460, 1994
A;Title: A luxAB transcriptional fusion to the cryptic celf gene of Escherichia coli dis A;Reference number: 542587; MUID:94166755
A;Accession: 542587
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C;Superfamily: fructose phosphotransferase multiphosphoryltransfer protein; phosphotrans
sphotransferase system phosphohistidine-containing protein homology
                                                                                                                                                         A, Note: the sequence of the natural peptide was confirmed by the synthesis and analysis C; Superfamily: bradykinin-potentiating peptide C; Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venc F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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R;de Crecy-Lagard, V.; Bouvet, O.M.M.; Lejeune, P.; Danchin, A.
J. Biol. Cham. 266, 18154-18161, 1991
A;Title: Fructose catabolism in Xanthomonas campestris pv. campestris. Sequence of A;Reference number: A40944; MUID:92011547
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Pred. No. 1.7e+03;
0; Mismatches 2;
R;Kato, H.; Suzuki, T.
Proc. Jpn. Acad. 46, 176-181, 1970
A;Reference number: A01254
                                                                                                                                                                                                                                                                                                                           Query Match 24.4%;
Best Local Similarity 66.7%;
Matches 4; Conservative
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A; Residues: 1-11 <GUZ>
C; Genetics:
A; Gene: celF
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A; Residues: 1-14 <DE3>
                                                                               A; Accession: A01254
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7 EAQREG 12
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Fondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocy, O. Blochemistry 10, 4033-4039, 1971

Biochemistry 10, 4033-4039, 1971

A; Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. I A; Reference number: A90356; MUID:72118526

A; Accession: A01253

A; Molecule type: Drotein

A; Residues: 1-13 < CND>

A; Note: the structure of the peptide was confirmed by synthesis

C; Comment: This peptide also potentiates bradykinin by inhibiting the kinases that inact C; Superfamily: bradykinin-potentiating peptide

C; Superfamily: bradykinin-potentiating peptide

C; Superfamily: angiotensin-converting enzyme inhibitor; pyroglutamic acid

E; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Oreste, U.; Coscia, M.R.; Scotto d'Abusco, A.; Santonastaso, V.; Ruffilli, A. Int. Arch. Allergy Appl. Immunol. 96, 19-27, 1991
A;Title: Purification and characterization of Par o I, major allergen of Parietaria offi A;Reference number: A53252; MUID:92091083
A;Accession: A53252
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C;Species: Bothrops jararaca (jararaca)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C;Accession: A01253
                                                                                                                                                                                                                                                                                                                                                            pollen major allergen Par o I - Parietaria officinalis (fragment)
C;Species: Parietaria officinalis
C;Date: 02-May.1994 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C;Accession: A53252
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A;Molecule type: protein
A;Residues: 1-12 <ORE>
A;Note: sequence extracted from NCBI backbone (NCBIP:72155)
A;Note: 5-Thr, 8-Asp, and 9-Ile were also found
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Job time: 167 sec
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C; Keywords: mitochondrion
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:39:28 ; Search time 12.32 Seconds (without alignments) 41.940 Million cell updates/sec Run on:

US-08-765-837-5 86 1 ENQRQGAEPRKNFVKP 16 Title: Perfect score: Sequence:

Scoring table:

88757 seqs, 32294092 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

111 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ipt	32 zea may	4 leucophae	P55235 spinacia ol	4	P30424 bothrops in	P18651 canis famil	~	P01021 agkistrodon			J	m					P41865 calliphora				068928 salmonella					P81532 microplitis	P12665 cricetidae	P80622 zea mays (m	\sim	P38498 procambarus	P82152 cydia pomon	æ	P41487 homarus ame
SUMMARIES	QI	UC26_MAIZE	BP37_LEUMA	GLGS_SPIOL	UC28_MAIZE	BPP4_BOTIN	FGF1_CANFA	CXA1_CONEP	BPPB_AGKHA	YMTP_XANCP	BPP1_BOTJA	LPAA_PORGI	LEC3_AXIPO	SCOT_RAT	RS7_MYCIT	FAR1_CALVO	FAR4_CALVO	FARA_CALVO	LMT1_LOCMI	CHI1_PEA	FAR4_PANRE	RS10_SALTY	RS10_SERMA	AMPN_HELAM	TKN_PHYFU	FARI_CALVO		IRBP_CRISP	UC16_MAIZE	FAR1_PROCL	FAR2_PROCL	ALL1_CYDPO	FAR3_HOMAM	FAR4_HOMAM
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ď	Query Match Length	30.	26.7	26.7	26.7	25.6	25.6	25.6	24.4	24.4	23.3	23.3	23.3	23.3	22.1	22.1	22.1	22.1	22.1	22.1	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.9	19.8	19.8	19.8	19.8	19.8
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TISSUE=BRAIN;
MEDLINE=97269266; PubMed=911447;
Muren J.E., Naessel D.R.;
"Seven tachykinin-related peptides isolated from the brain of the madeira cockroach; evidence for tissue-specific expression of

SEQUENCE, AND MASS SPECTROMETRY.

30-MXY-2000 (Rel. 39, Created)
30-MXY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Leucophaea maderae (Madelra cockroach).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda: Insecta; Plerygota; Neoptera: Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.

13 AA.

PRT;

STANDARD;

BP37_LEUMA P81754;

RESULT 2 BP37_LEUMA

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UHO9_RAT FAR2_CALVO FAR3_CALVO LADD_ONCMY OWL_PSEGU CXAA_CONST FARB_ASCSU UP5L_UPEIN EFTU_CANFA RS19_PPWBP	ALIGNMENTS	PRT; 8	01-OCT-1996 (Rel. 34, Created) 10-OCT-1996 (Rel. 34, Last sequence update) 11-JUL-1999 (Rel. 38, Last annotation update) 12-JUL-1999 (Rel. 38, Last annotation update) 12-JUL-1999 (Rel. 38, Last annotation update) 13-JUL-1999 (Rel. 38, Last annotation update) 13-JUL-1999 (Rel. 38, Last annotation update) 13-JUL-1999 (Rel. 38, Last annotation update) 14-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 16-JUL-1999 (Rel. 38, Last annotation update) 17-JUL-1999 (Rel. 38, Last annotation update) 18-JUL-1999 (Rel. 38, Last annotation u	2D-GEL THE DETERNI XM IS: 57.2 KDA. SOPTILE. 9639D6DAB4176B1D ; SCORE 26; DB 1 ; Pred. NO. 8.9e+ 0; Mismatches
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		STANDARD;	(Rel. 34, Creat (Rel. 38, Last (Rel. 38, Last (Rel. 38, D-PA ize). (Inidiplantae; E itidiplantae; E itidiplant	Dr. Appl. Genet. 93:997-1005(1996) MISCELLANEOUS: ON THE 2D-GEL THE PROTEIR IS: 7.0, ITS WM IS: 57.2 ITER 8 8 8 IENCE 8 AA; 990 MM; 9639D6DAB4 BACC
11 12 13 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16	-	MAIZE UC26_MAIZE	01-OCT-1996 (Rel. 34, Creat Ol-OCT-1996 (Rel. 34, Last 15-JUL-1999 (Rel. 38, Last UNKNOWN PROTEIN FROM 2D-PAC (FRAGMENT). (FRAGMENT). (FRAGMENT). (ERAGMENT). (ERAGMENT). (ENACYOLE, VIITIDIPAITAE; EMAGNOLIOPHYTA; LILIOPSIDA; FOUR AMAGNOLIOPHYTA; LILIOPSIDA; FOUR AMAGNOLIOPHYTA; LILIOPSIDA; FOUR AMAGNOLIOPHYTA; COUR AMAGNOLIOPHYTA; COUR AMAGNOLIOPHYTA; COUR AMAGNOLIOPHYTA; TOWA COUR AMAGNOLIOPHYTA; TOWA COUR AMAGNOLIOPHYTA; TOWA COUR AMAGNOLIOPHYTA; COUR AMAGNOLIO	SON NIS
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Spermatophyta;

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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
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Cintra A.C.O., Vieira C.A., Giglio J.R.;
Cintra A.C.C., Vieira C.A., Giglio J.R.;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
Frimary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227(1990).
-I- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTIVITY OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
PIR. D37196. D37196.
                                                                                                                                                                                                                                                              Theor. Appl. Genet. 9397-1005(1996).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.2, ITS MW IS: 27.7 KDA.
MAIZE-2DRAGE: P80634; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops
   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
BRADYKNIN-POTEMTIATING FEPTIDE $4,1,2 (ANGIOTENSIN-CONVERTING FRIZYME INHIBITOR).
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                                                                                          Zea mays (Maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
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Pred. No. 4.2e+02;
0; Mismatches 2;
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ilarity 66.7%;
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P30424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GLUGOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT (EC 2.7.7.2)
(ADP-GLUGOSE SYMTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B)
(ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBCELLUIAR LOCATION: CHLOROPLASTS OF LEAVES AND AMYLOPLASTS OF DEVELOPING ENDOSPERM.
-:- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-PHOSPHATE ADEMYLYLTRANSFERASE FAMILY.
                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO, IPRO1825, -.
PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; PARTIAL.
PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; PARTIAL.
PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; PARTIAL.
Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
Multigene family; Starch biosynthesis; Allosteric enzyme;
Amyloplast; Chloroplast.
                                                                                                                           Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 14;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
isoforms.";
Peptides 18:7-15(1997).
Peptides SPECIFICITY: BRAIN.
-!- TISSUE SPECIFICITY: BRAIN.
-!- MASS SPECTROMETRY: MW=1435.7; METHOD=MALDI-MS.
SEQUENCE 13 AA; 1436 MW; 8E532C9DE9A7D1B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AA; 1490 MW; 98B5792C3AE738C5 CRC64;
                                                                                                                         Score 23; DB 1; Le
Pred. No. 3.4e+02;
); Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 1; Le
Pred. No. 3.6e+02;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                      14 AA.
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                                                                                                                         26.7%;
50.0%;
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33.3%;
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.7
Best Local Similarity 33.3
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                              ENQRQGAEPR 10
                                                                                                                                                                                                                               4 EESTVSAEPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : | : |
5 QNSQDGLDP 13
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UC28_MAIZE
ID UC28_MAIZE
AC P80634;
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P55235:
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SEQUENCE
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Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidailon; Venom; Sulfatation; 3D-structure. DISULFID \frac{2}{1000}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffil).
Bukaryota; Metazoca; Chordata; Craniata; Vertebrata; Euceleosiumi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Amino acid sequence of bradykinin-potentiating peptide isolation venom of Agkistrodon halys blomhoffii.";

Proc. Jpn. Acad., B. Phys. Biol. Sci. 46:176-181(1970)
-!- FUNCTION: THIS PEPTIDE BOTH INIBIRTS THE ACTIVITY UP THE BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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15-JUL-1998 (Rel. 36, Last annotation update)
BRADYKININ-POTENTIATING PEPTIDE B (ANGIOTENSIN-CONVERTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21; DB 1; Length 11; Pred. No. 6.38+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                    Score 22; DB 1; Lenyth 16;
pred. No. 6.2e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID. 295CBF0627741777 CRC64;
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MEDLINE-92011547; PubMed-1655739;
de Crecy-Lagard V., Bouvet O.M., Lejeune P., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
HYPOTHETICAL PROTEIN IN FRUK 5'REGION (ORF1) (FRAGMENT).
                                                                                                                                    AMIDATION.
C63385F376C99B4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA.
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                                                                                                            SULFATATION
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66.78;
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40.0%;
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16
15
16
1792 MW;
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                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kato H., Suzuki T.;
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         4 SDPRCNMNNP 13
                                                             2
3
15
16
16 AA;
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1 QGLPPR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas.
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Q03397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BPPB_AGKHA
                                                                                                                                    MOD_RES
SEQUENCE
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                                                                                  DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethe N., Sharma H.S., Schaper W.; "Isolation of heparin-binding growth factors from bovine, porcine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBUNIT: MONOMER.
-i- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY. PIR: $03955; $03955. HSSP: $03955. HSSP: $03955. POS.209. AND THE PRODUCTORS FAMILY. INTERPRO: IPRO02209; -PROSITE; PS00247; HBGF_FGF; PARTIAL. Growth factor; Mitogen; Vascularization; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
11-OCT-1996 (Rel. 34, Last annotation update)
12-OCT-1996 (Rel. 34, Last annotation update)
13-OCT-1996 (Rel. 34, Last annotation update)
14-OCT-1996 (Rel. 34, Last annotation update)
15-OCT-1996 (Rel. 34, Last annotation update)
16-OCT-1996 (Rel. 34, Last annotation u
                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     canine hearts.";

Eur. J. Biochem. 181:67-73(1989).

-!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIGGENIC

IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES
VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CONCENTRATION OF THESE 2 GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 1; Length 15; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AA; 1732 MW; 53CC9A3CADDDDAA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 AA.
                                                                                  15 AA.
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                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89231704; PubMed-2714282;
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60.0%;
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                                                                                  STANDARD;
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PDB; 1AOM; 13-JAN-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA-CONOTOXIN EPI.
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Best Local Similarity
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1 NYMKP 5
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P56638;
                                                                                  FGF1_CANFA
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SEQUENCE
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SEQUENCE.
                                                       FGF1_CANFA
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Indels

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STRAIN-W50;
MEDLINE-99061194; PubMed=9846737;
MEDLINE-99061194; Reddi K., Fletcher J., Nair S., Wilson M.,
Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
Curtis M., Henderson B., Tabona P.;
"A lipid A-associated protein of Porphyromonas gingivalis, derived
from the haemagglutinating domain of the RI protease gene family, is
a potent stimulator of interleukin 6 synthesis.";
Microbiology 144:3019-3026(1998).
-: FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID
THAT ANCHORS THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE (A: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Axinella polypoides (Sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
Halichondrida; Axinellidae; Axinella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 1; Length 13;
Pred. No. 1.1e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38EA796EAFA63AB7 CRC64;
                                                                                                                                                                                                                                                                LIPID-A-ASSOCIATED PROTEIN (FRAGMENT).
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidaceae; Porphyromonas.
                                                                                                                                                                                                           (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
                                                                                                                                                                         13 AA.
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   Mismatches
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                                                                                                                                                                         PRT;
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50.0%;
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15 AA; 1744 MW;
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 Conservative
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13
13 AA;
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Best Local Similarity
Matches 4; Conserv
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                                     5 QGAEPR 10
                                                                 1 OGGWPR
                                                                                                                                                                                                             15-DEC-1998
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                                                                                                                                                                                                                                                15-DEC-1998
   4
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P81411;
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LEC3_AXIPO
ID LEC3_AXIPO
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SEQUENCE
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SEQUENCE
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SEQUENCE.
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                                                                                                                                    RESULT 11
LPAA_PORGI
 Matches
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                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
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                 Sequence of the PTS operon, characterization of the fructose-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-B.INSULARIS; TISSUE-VENOM;
MEDLINE-90351557; PubMed=2386615;
Cintra A.C.O., Vielra C.A., Giglio J.R.;
Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227(1990).
-!- FONGTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Anglotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis."; Biochemistry 10:4033-4039(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BPPI_BOTJA STANDARD; PRT; 13 AA.
P01020; P30421;
21-JUL-1986 (Rel. 01, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
BRADYKININ-POTENTIATING PEPTIDE S3,1 (13A) (ANGIOTENSIN-CONVERTING ENZYME INHIBITOR V-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bothrops jararaca (Jararaca), and
Bothrops insularis (Island jararaca) (Queimada jararaca).
Eukaryota: Metazoca; Chordata; Craniata; Vertebrata; Euteleostomi;
Leptdosauria; Squamata; Soleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                      ;
 campestris.
                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 1; Length 14;
Pred. No. 8.1e+02;
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                                                                                                                                                                                                                                                                                                                         72EA9AA3CE16CCDB CRC64;
"Fructose catabolism in Xanthomonas campestris pv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 1; I
Pred. No. 1.1e+03;
                                                   Biol. Chem. 266:18154-18161(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-B.JARARACA; TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=72118526; PubMed=4334402
                                                                                                                                                                                                                                        EMBL; M69242; AAA27600.1; -. PIR; C40944; C40944.
                                                                                                                                                                                                                                                                                                                       14 AA; 1585 MW;
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66.78;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypotensive agent; Venom. MOD_RES 1 1 1 SEQUENCE 13 AA; 1388 MW
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A01253; XAVI9B.
PIR; A37196; A37196.
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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7 EAQREG 12
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Gaps

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Score 20; DB 1; Length 15; Pred. No. 1.3e+03;
DC05E47E3F8DC5F3 CRC64;
                                             23.3%;
                                                            Best Local Similarity
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Nucleic Acids Res. 21:1039-1039(1993).
-!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
16S RIBOSOMAL RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROFEINS.
                                                                                                                                                                                                                                                                                       835538; 835538
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Best Local Similarity
Matches 2; Conserv
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les 3; Conserv
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2 PQQDFMR 8
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2 RKGPAPK
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ID FARI_CALVO
AC P41856;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND SYNTHESIS.
MEDLINE=72240741; Pubmed=4558348;
Ungar G., Desiderio D.M., Parr W.;
Isolation, identification and synthesis of a specific-behaviour-inducing brain peptide.";
Nature 238:198-202(1972).
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"Nucleotide sequence analysis of the ribosomal S12 gene of
Mycobacterium intracellulare.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 1; Length 15;
Pred. No. 1.3e+03;
2; Mismatches 1; Indels
      Indels
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5B87696F6C7FD76C CRC64;
    5
                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
30S RIBOSOMAL PROTEIN S7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comments on the chemistry of scotophobin.";
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                                                                                                                                                                                   15 AA.
    Mismatches
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J. Chem. Soc. Chem. Commun. 432-433(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ungar G., Desiderio D.M., Parr W.;
Nature 238:209-210(1972).
-!- TISSUE SPECIFICITY: BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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MEDLINE=72240742; PubMed=4558349;
    5;
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50.0%;
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15 AA; 1582 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 238:202-209(1972).
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Matches 3; Conservative
    3; Conservative
                                                                                                                                                                                   STANDARD;
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                                         7 AEPRKNF 13
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1 ASPXENY 7
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2 DNNQQG
                                                                                                                                                                                                                                                                                   SCOTOPHOBIN.
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P33564;
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SEQUENCE
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P01159;
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    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 8.9e+04;
5; Mismatches 0; Indels
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29D00699CAB6C6C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                850 MW; 63276DC768732417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFMREANIDE 1.
Calliphora vomitoria (Blue blowfly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA.
                                                                                                                                                                                                                                                       PROSITE; PSGUUJZ; ALLOCALING RIBOSOMAL protein; FRNA-binding.

0 BY SIMILARITY.
                                                                                                                                                                                                                             INTERPRO; IPR000235; -. PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                     EMBL; L08171; AAA25376.1; -.
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Similarity 28.68;
2; Conservative
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MOD_RES 9 9
SEQUENCE 9 AA; 1169 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Q83171 cauliflow

090469 drosophila 010234 human immun 010226 human immun 010227 human immun 010229 human immun 010239 human immun 010230 human immun 010233 human immun 010233 human immun 010235 human immun 010235 human immun 010235 human immun 010237 human immun 010237 human immun 010238 human immun 010239 human immun 010239 human immun 010231 human immun 010231 human immun 010231 human immun 010231 human immun 010233 human immun 010234 human immun 010234 human immun 010235 human immun 010235 human immun 010239 human immun 02240 human

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112 113 113 113 113 113 114 115 116 117

Q9TWK0 Q53914 Q9QVE7 Q9JLI5 O90348

micrococcus homo sapien streptococc spinacia ol

Q9r596 r Q07059 021922 Q9t2Fi

054298 P82331 Q9R596 Q07059 021922

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PS PROUECE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-MONTEMAYOR;

XA MEDLINE-98393576; PubMed-9725836;

XA Ramos-orasins S., Aguade M.;

**Manos-orasins S., Aguade M.;

**Molecular evolution of the Cecropin multigene family in Drosophila:

**T unctional genes vs pseudogenes.";

**Genetics 150:157-171 (1998).

C -1- FUNCTION: MALE-SPECIFIC PEPTIDE WITH MODERATE ACTIVITY AGAINST

CC -1- SIMILARITY: STRUCTUGRALLY RELATED TO CECROPINS.

CRAM-POSITIVE BACTERIA (BY SIMILARITY).

CC -1- SIMILARITY: STRUCTUGRALLY RELATED TO CECROPINS.

CC -1- SIMILARITY: DSEC\Anp.

CC -1- SIMILARITY: Antibiotic.
                                                                                                                                                                                                                                                                                                                                               Drosophila sechellia (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TAXID=7238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.9%;
40.0%;
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
ANDROPIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
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AKPIENMILP 10
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01-MAY-1999
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                              P81687;
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P81687
RESULT
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Q8R772 simian hemo
Q9k977 simian hemo
Q9k973 spinacia ol
Q6531 mus spretus
P82597 bacillus sp
Q9kc50 bacillus ha
Q9mrz hemo saplen
Q62207 mus musculu
Q62207 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09qv76 mus sp. pre
09ps10 gallus gall
088082 chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9mqk3 capra ibex
Q63940 rattus norv
                                                                   (without alignments)
57.262 Million cell updates/sec
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Q14804 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bos taurus
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                                                         Search time 32.75 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9tqz9 :
Q9trb4 ]
                                                                                                                                                                       2612
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                      374700 segs, 117207915 residues
                                                         January 17, 2001, 13:39:12;
                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 1008
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Q14804
Q9TQ29
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Q68772
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P82597
Q9KC50
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Q63940
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P82135
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sp_bacteria:*
sp_lungi:*
sp_lungan:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
                                                                                                           1 ENORGGAEPRKNFVKP 16
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sp_vertebrate:*
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86
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Last sequence update) Last annotation update)

Created)

08, 10,

11 AA.

ALIGNMENTS

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Gaps 0;

Score 24; DB 5; Length 11; Pred. No. 7.8e+02; 3; Mismatches 3; Indels

OB6F902556944B10 CRC64;

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NCBI_TaxID=9913;
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01-MAY-2000 (TIEMBLICEL. 13, Last sequence update)
01-JUN-2000 (TIEMBLICEL. 14, Last annotation update)
01-JUN-2000 (TIEMBLICEL. 14, Last annotation update)
20 KDA PHOSPHOKTATION-DEPENDENT PROTEIN PHOSPHATASE-1 INHIBITORY
SUS SCOFÉM (PIQ).
EURATYOTA; MCLAZOA; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eto M., Ohmori T., Suzuki M., Furuya K., Morita F.;
"A novel protein phosphatase-1 inhibitory protein potentiated by
protein kinase C. Isolation from porcine aorta media and
characterization.";
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Pred. No. 9.3e+02;
2; Mismatches 2; Indels
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                                                                                                                                                                                                          13 AA; 1530 MW; 9DC880B73FCD16C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biochem. 118:1104-1107(1995).
SEQUENCE 16 AA; 1822 MW; 7711966667B09400 CRC64;
                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%; Score 24; DB 6; Ler ilarity 57.1%; Pred. No. 1.1e+03; Conservative 2; Mismatches 1;
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         13 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last seq:
                                                      CHLORIDE CHANNEL PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                           PRT;
         PRT;
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MEDLINE-95050513; Pubmed~7961681;
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                                                                                                                                                                                                                                    27.9%;
50.0%;
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         PRELIMINARY;
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                                                                         Homo sapiens (Human)
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Best Local Similarity
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Best Local Similarity
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5 QSQRHGGE 12
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                                                                                                     NCBI_TaxID=9606;
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PTENFVQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.; "Molecular characterization of six intermediate proteins in the processing of mouse protamine P2 precursor."; Eur. J. Blochem. 204:759-755(1992). SEQUENCE 10 AA; 1028 MW; 2B099C75B72866DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 6; Length 10, Pred. No. 1.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                     family.";
J. Biol. Chem. 269:20878-20884(1994).
SEQUENCE 16 AA; 1878 MW; F70F74211EE26EDE CRC64;
01-JUN-2000 (TrEMBLrel. 14, Last annotation update) ATP-DEPENDENT 20 S PROTEASCME ACTIVATOR (FRAGMENT).
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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                                                                                                                                                                                                                                                     MEDLINE=94342244; PubMed=8063704;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                        Bovidae; Bovinae; Bos
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Nadeau J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
Mamm. Genome 5:349-355(1994).
--- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND MURE.
SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
EMBL; U05696; AAA61936.1, -.
Calcium-binding; Placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
THERMOSTABLE MONOACYLGLYCEROL LIPASE (MGLP) (24 KDA) (EC 3.11.23)
 -i- MISCELLANEOUS: S18 ALPHA AND BETA FORMS DIFFER IN Pl. S18 BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10096;
                  FORM IS THE LEAST BASIC FORM.
-!- SIMILARITY: BELONGS TO THE SIBP FAMILY OF RIBOSOMAL PROTEINS.
INTERPRO; IPRO01648; --
PROSITE; PS00057; RIBOSOMAL_S18; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PLACENTAL CALCTUM-BINDING PROFIEIN (18A2) (PEL98) (WTSI PROFIEIN)
(METASTATIC CELL PROTEIN) (FRAGMENT).
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                                                                                                                                                                                                                   4; Indels
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15 AA; 1910 MW; C29396F592403B60 CRC64;
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2.4e+03;
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                                                                                                                                                                              Score 22; DB 8; I
Pred. No. 2.4e+03;
5; Mismatches 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SPRET/EI;
MEDLINE=94319082; Pubmed=8043949;
                                                                                        Ribosomal protein; Chloroplast.
                                                                                                                                                                               25.6%;
30.8%;
                                                                                                                                                                               Query Match 25.6
Best Local Similarity 30.8
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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|1 EPRK 14
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CHLOROPLAST 30S RIBOSOWAL PROTEIN S18 ALPHA (FRAGMENT).
Spinacia oleracea (Spinach).
Chloroplast.
Eukaryota, viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Garyophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID-3562;
            Zeng L., Godeny E.K., Methven S.L., Brinton M.A.;
"Analysis of simian hemorrhagic fever virus (SHFV) subgenomic RNAs,
junction sequences, and 5' leader.";
Virology 207:543-548(1995).
EMBL: L39091; AAA68933.1;
NON_TER 12 12
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-1: SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
-1: TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
                                                                                                                                                                               Length 12;
                                                                                                                                                             Score 22; DB 12; Length 12
Pred. No. 1.9e+03;
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Pred. No. 2.1e+03;
1; Mismatches 2; Indels
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STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EmBL/GenBank/DDBJ databases.
EMBL; AP001516; BAB06430.1; -...
SEQUENCE 13 AA; 1606 MW; CAE02359F55A25B9 CRC64;
                                                                                                       NON_TER 12 12
SEQUENCE 12 AA; 1398 MW; 88911EA56CA4176E CRC64;
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Last annotation update)
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NCBL_TaxID=86665;
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MEDLINE-95193253; PubMed-7886957;
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66.7%;
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Best Local Similarity 57.1
Best Local 4; Conservative
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Bacillus halodurans.
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Matches 4; Conserv
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RESULT P82135

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TISSUE=BRAIN;
MEDLINE=95072570; PubMed=7981675;
Huynh D.P., Nechiporuk T., Pulst S.M.;
"Alternative transcripts in the mouse neurofibromatosis type 2 (NF2)
gene are conserved and code for schwannomins with distinct C-torminal domains.";
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                                                                                                 "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
that are associated with differences in platelet alpha2 betal
density "
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                  SEQUENCE FROM N.A.
MEDLINE-99421383; PubMed-9746778;
Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
Kunicki T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.4%; Score 21; DB 11; Length 11; 57.1%; Pred. No. 2.6e+03;
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Pred. No. 2.6e+03;
1; Mismatches 2; Indels
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Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ENVELOPE GIXCOPROTEIN.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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EMBL; L28838; AAA57151.1; -.
MGD; MGI:97307; Nf2.
                                                                                                                                      density.";
Blood 92:2382-2388(1998).
EMBL; AF062039; AAF77577.1; -.
NON_TER 16 16
SEQUENCE 16 AA; 1635 MW; F6
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Similarity 57.1%;
4; Conservative
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001512; BAB05443.1; -
SEQUENCE 16 AA; 1836 MW; 4A121EFC8CBC9DBA CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
INTEGRIN ALPHA-Z SUBUNIT (FRAGMENT).
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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Pred. No. 2.6e+03;
0; Mismatches 1;
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NCBI_TaxID=86665;
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              MEDLINE=20198254; PubMed=10731713;
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SEQUENCE FROM N.A.
STRAIN=546CP-H7, 546CP-E4, AND 546CP-F5; TISSUE=CHOROID PLEXUS;
Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
Analysis of human immunodeficiency virus type 1 gp160 sequences from a patient with HIV dementia: evidence for monocyte trafficking into brain.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                   Query Match 24.4%; Score 21; DB 12; Length 12; Best Local Similarity 66.7%; Pred. No. 2.9e+03; Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                           D. Neurovirol. 0:0-0(2000).

EMBL; AF217155; AAF75497.1; -.

EMBL; AF217154; AAF75495.1; -.

EMBL; AF217154; AAF75496.1; -.

SEQUENCE 12 AA; 1636 MW; 7ED6A2917A24005B CRC64;
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FEBS Lett. 322:219-222(1993).
SEQUENCE 15 AA; 1600 MW; 70E3C05B5D004017 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PREGNANCY ASSOCIATED MOUSE PROTEIN 1 (FRAGMENT).
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SEQUENCE.
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AC 090V76;
DT 01-MAY-
DT 01-MAY-
DT 01-MAY-
DT 01-MAY-
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Sequence 3, 7

App i Appl

Sequence 1, Al Sequence 1, Al Sequence 19, Sequence 20, Sequence 40, Sequence 11, Al

US-09-172-019-5
US-09-16-094-5
US-08-474-587-3
US-08-474-587-3
US-08-149-809-7
US-08-152-951-19
US-08-572-951-19
US-08-572-951-19
US-08-572-951-10
US-08-572-951-40
US-08-572-951-40
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US-08-572-951-40
US-08-572-951-40
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US-08-957-264-7

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Sequence 1, Sequence 7, Sequence 8,

Appl1 Appl1 Appl1 Appl1 Appl1

Sequence 7, Sequence 8, Sequence 3,

ALIGNMENTS

us-08-765-837-5.closed.rai

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APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INITIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERNCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                     Sequence 41, Application US/09016366A Patent No. 5955431 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOSCON
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALLISE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
Matches 5; Conserv
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 Sequence 110, App
Sequence 110, App
Sequence 2, Appli
Sequence 5, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 68,
Sequence 6,
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Sequence 7,
Sequence 6,
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Sequence 6
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                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-463-620-7

US-08-224-917-7

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US-08-914-853-6

US-08-914-853-6

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US-08-477-877B-31

US-08-477-877B-31

US-08-477-878B-31

US-08-477-89B-31

US-08-470-28B-31

US-08-750-359-3

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US-08-750-359-3

US-08-750-359-3

US-08-871-355-110

US-08-871-358-110

US-08-85-3578-10

US-08-83-148-15

US-08-83-1358-110

US-08-83-1358-110

US-08-83-1358-110

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                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                               174772 seqs, 17957048 residues
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                                                                             January 17, 2001, 13:37:03
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                           US-08-765-837-5
86
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Match Length
                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                             Scoring table:
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Indels Length 8;

Score 30; DB 2; L6 Pred. No. 1.3e+05; 2; Mismatches 1;

34.9%; 62.5%;

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TYPE: amino actu
STRANDEDNESS: single
      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FRAGMENT TYPE:
US-08-463-620-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-463-620-7
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                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBLOUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBLOUITIN-CONJUGATING ENZYME
FILE REPERBNCE: 0-5359
CURRENT FILING DATE: 1999-03-22
EARLIER PILING DATE: 1998-04-07
EARLIER PILING DATE: 1998-04-07
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER POFICATION NUMBER: JP 69163/1997
EARLIER POFICATION NUMBER: JP 69163/1997
EARLIER POFICATION NUMBER: JP 69163/1997
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Sequence 6, Application US/08463620
Fatent No. 5789216
Fatent Fatent Jimmy Wayne
Fitte OF INVENTION: Cloning and Expression of Human GMP
FITLE OF INVENTION: Synthetase, its use in Screening for Inhibitors of
FITLE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Syntheta
FATENTLE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Syntheta
CORRESPONDENCE ADDRESS:
FATENTE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Syntheta
CORRESPONDENCE ADDRESS:
FATENTE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
FATENTE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
FATENTE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
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FATENTE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
FATENTE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
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Pred. No. 31;
1; Mismatches 6; Indels
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CURRENT APPLICATION DATA:
RELICATION NUMBER: US/08/463,620
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            Sequence 68, Application US/09273565A
Patent No. 6166190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Syntex (USA) Inc. STREET: 3401 Hillview Avenue CITY: Palo Alto STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.98;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ORQGAEPRKNFVK 15
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bovine sp.
US-09-273-565-68
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Best Local Similarity
Matches 6; Conserv
3 QRQGAEPR 10
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1 QKRGREPR 8
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US-09-273-565-68
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APPLICANT: Lou, Lillian Lien-Li
APPLICANT: Barnett, Jimmy Wayne
TITLE OF INVENTION: Cloning and Expression of Human GMP
TITLE OF INVENTION: Stoning and Expression of Human GMP
TITLE OF INVENTION: Human
TITLE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthrese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/463,620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30;
Pred. No.
US 08/224,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,917
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                      REFERENCE/DOCKET NUMBER: 28060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-852-1698
TELEFAX: (415)-496-3529
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,752
REFERENCE/DOCKET NUMBER: 28060
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 7, Application US/08463620
; Patent No. 5789216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Syntex (USA) Inc. 3401 Hillview Avenue
                                                                NAME: Peries, Rohan
REGISTRATION NUMBER: 35,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.9%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415)-852-1698
                      FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Peries, Rohan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415)-496-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.9
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                         . peptide
NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     internal
                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3401 Hilly CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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3 EPLKDFIK 10
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%5-08-914-853-6
; Sequence 6, Application US/08914853
; Patent No. 5998186
    7, Application US/08224917
                                                                                                                                                                                             ADDRESSEE: Syntex (USA) Inc.
STREET: 3401 Hillview Avenue
CITY: Palo Alto
STATE: California
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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    Sequence 7, Application Patent No. 5965350 GENERAL INFORMATION:
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3 EPLKDFIK 10
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; FRAGMENT TYPE:
US-08-224-917-7
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                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08224917
Patent No. 5965350
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lou, Lillian Lien-Li
APPLICANT: Barnett, Jimmy Wayne
TITLE OF INVENTION: Cloning and Expression of Human GMP
TITLE OF INVENTION: Synthetase, its use in Screening for Inhibitors of Human
TITLE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: Syntex (USA) Inc.
STREET: 3401 Hillview Avenue
CITY: Palo Alto
STATE: California
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Pred. No. 34;
2; Mismatches 1; Indels
                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUNTE: CALLICETIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,917
FILING DATE: 08-APPR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: PETIES, ROHAN
REGISTRATION NUMBER: 35,752
REFERENCE/DOCKET NUMBER: 28060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,-852-1698
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.9
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                           5; Conservative
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                    ; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-463-620-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
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TOPOLOGY: linear
                                                                                                                                                    Best Local Similarity
Matches 5; Conserv
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US-08-224-917-6
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US-08-224-917-7

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PREMILE NO. 5993-304

PREMILE NO. 5993-304

PREMILE BETTHEL JIAN LIGHT. LIGHT.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-852-1698
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                             Best Local Similarity 62.5
Matches 5; Conservative
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NO
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Best Local Similarity
'...hos 5; Conserv?
                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                 linear
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3 EPLKDFIK 10
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                                                                                                                                                 TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                    FRAGMENT TYPE:
US-08-914-853-7
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FRAGMENT TYPE:
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GMP Synthetase and Inhibitors of Human GMP Synthetase
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LOU, Lillian Lien-Li
APPLICANT: Barnett, Jimmy Wayne
TITLE OF INVENTION: Cloning and Expression of Human GMP
TITLE OF INVENTION: Synthetase, its use in Screening for Inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 14;
             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.9%; Score 30; DB 62.5%; Pred. No. 34; Live 2; Mismatches
                                                                     APPLICATION NUMBER: US/08/914,853 FILING DATE: CLASSIFICATION:
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,489
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Peries, Rohan
REGISTRATION NUMBER: 35,752
REPERENCE/DOCKET NUMBER: 28060
TELECOMUNICATION INFORMATION:
TELEPHONE: (415)-852-1698
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08914853
Patent No. 5998186
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Syntex (USA) Inc. 3401 Hillview Avenue
 COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING EVENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *NAME: Peries, Rohan REGISTRATION NUMBER: 35,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.9
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSE: Syntex (U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 EPRKNFVK 15
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3 EPLKDFIK 10
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-914-853-6
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Sequence 6, Application PC/TUS9503934A
GENERAL IMPORMATION:
APPLICANT: Syntex (USA) Inc.
TITLE OF INVENTION: Cloning and Expression of Human GMP
TITLE OF INVENTION: Synthetase, its use in Screening for Inhibitors of Human
TITLE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FCT-US95-03934A-7; Sequence 7, Application PC/TUS9503934A; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Syntex (USA) Inc.
TITLE OF INVENTION: Cloning and Expression of Human GMP
TITLE OF INVENTION: Synthetase, its use in Screening for Inhibitors of Human; TITLE OF INVENTION: GMP Synthetase and Inhibitors of Human GMP Synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03934A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 34;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    34.9%; Score 30; 62.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30;
Pred. No.
TELEFAX: (415)-496-3529
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                          LENGTH: 14 amino acids
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NESOLA 12-281A-31
Sequence 31, Application US/08472281A
Sequence 31, Application US/08472281A
Sequence 31, Application US/08472281A
Sequence 31, Application US/08472281A
SERERA INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
STRET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
STATE: New Jersey
COUNTRY: ISA BAJABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
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                                                             Score 28; DB 1; Length 15; Pred. No. 80;
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                                                                                                      Indels
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Pred. No. 80;
1; Mismatches 3
                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MR-1995
APPLICATION NUMBER: 08/119,032
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Olstein, Elliot M.
REGISTATION UNDRER: 24,025
REPERENCE/DOCKET NUMBER: 6175
RELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1740
INFORMATION FOR SEQ ID NO: 31:
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nilarity 55.6%;
Conservative
                                                             32.6%;
55.6%;
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                                        Query Match
Best Local Similarity 55.0.
Fra 5; Conservative
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LENGTH: 15 amino acids
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Best Local Similarity
Lass 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                             3 QRQGAEPRK 11
                                                                                                                                                                                     4 ORPGOSPRR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-477-989B-31
  US-08-477-877B-31
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APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Active
WUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cacchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STREET: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 4; Length 14; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: PCT/US95/03934A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 aming acids
                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18 ps/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/477,877B
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/19,032
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
REGISTRATION NUMBER: 24,025
RECISTRATION NUMBER: 24,025
RECISTRATION INBER: 24,025
RECISTRATION INBER: 61750-146
TELECOMMUNICATION INBER: 61750-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31. Application US/08477877B Patent No. 5730979 GENERAL INFORMATION:
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                         internal
                                                                                                                                                                                     single
                                                                                                                                                                                                                              peptide
                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
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3 EPLKDFIK 10
                                                                                                                                                                                                      TOPOLOGY: lin-
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
PCT-US95-03934A-7
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TRANSFORMANT CONTAININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA FRAGMENT ENCODING A POLYPEPTIDE HAVING NITRILE HYDRATASE ACTIVITY, A TRANSFORMANT CONTAIN GENE AND A PROCESS FOR THE PRODUCTION OF AMIDES USING THE TRANSFORMANT
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 2; Length 14, Pred. No. 1.18+02;
                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION RAIS-SOFTWARE: PATENTION NATA:
APPLICATION NUMBER: US/08/028,463
FILING DATE: 09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7005-023-999
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FILING DATE: 09-MAR-195,
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,747
FILING DATE: 02-MAY-1991
ATTORNEY AGGNT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
RECISTRATION NUMBER: 7005-023-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YAMADA, HIDEAKI
APPLICANT: NAGASAWA, TORU
APPLICANT: NISHIYAWA, MAKATO
TITLE OF INVENTION: DNA FRAGMENT
TITLE OF INVENTION: GENE AND A PR
TITLE OF INVENTION: GENE AND A PR
TITLE OF INVENTION: TRANSFORMANT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08028463 Patent No. 5731176
                                                                                                                                                                                                                                                    single stranded
                                                                                                                                                                                                                                                                                                                                                                           31.4%;
55.6%;
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  Floppy disk
                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single str
                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-750-359-3
                                                                                                                          FILING DATE:
CLASSIFICATION: 424
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Best Local Similarity
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  MEDIUM TYPE:
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US-08-028-463-11
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TITLE OF INVENTION: Monoclonal antibody against CD44v6
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
                                                                                                                                       APPLICANT: Postema, Christina E.
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
CORRESPONDENCE: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 2
Pred. No. 80;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM PS/2
CURSENT APPLICATION DATA:
APPLICATION NUMBER: 08/04/7,989B
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 109-MAR-1993
APPLICATION NUMBER: 24,025
REGISTRATION NUMBER: 24,025
REGISTRATION NUMBER: 61750-147
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Sequence 31, Application US/08477989B
                                                          Bazin, Herv
Latinne, Dominique
Kaplan, Ruth
Kieber-Emmons, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-750-359-3
; Sequence 3, Application US/08750359
; Patent No. 5916561
; GENERAL INFORMATION:
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55.6%;
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Best Local Similarity 55.0°,
Thes 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 6 |
CITY: Rose
                                                                                                                    APPLICANT:
                                                                                                  APPLICANT
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: TOPOLOGY: linear

MOLECULE TYPE: peptide

CORGANISM: Rhodococcus rhodochrous

STRAIN: J-1 (FERM BP-1478)

US-08-028-463-11

Query Match

Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 5; Indels

Qy 2 NONGAEPRRN 12

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Db 4 NPVQCTLPRXN 14
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0; Gaps

Search completed: January 17, 2001, 13:37:04 Job time: 124 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Search time 15.26 Seconds (without alignments) 29.130 Million cell updates/sec ٠. January 17, 2001, 13:25:20 Run on:

US-08-765-837-1 66 1 RTTLQSDQEEIDY 13 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

268485 seqs, 34193795 residues Searched:

92618 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_36:*

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/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:*

/SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*

/SIDS1/gcgdata/geneseq/geneseqp/Aa1993. DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/Aa1994. DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/Aa1995. DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/Aa1996. DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/Aa1997. DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/Aa1997. DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/Aa1999. DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/Aa1999. DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*

SUMMARIES

	Description	Factor VIII antide	Selectin based ant	ITIM motif used to	Fragment of SAll r	HLA binding peptid	HLA binding peptid	V8 fragment of CD4	Human munc13 (Hmun	DR3-restricted T-h	DR3-restricted T-h	Cytotoxic I lympho	Cytotoxic T lympho
	ID	R90945	R28967	W06271	P60552	Y07173	x07131	R82679	Y27136	R46053	R46057	R43245	R43246
	Query Match Length DB ID	13 17	13 13	13 17	12 7	10 20	10 20	11 16	13 20	7 15	7 15	8 14	8 14
æ	Query Match I	100.0	43.9	39.4	37.9	36.4	36.4	36.4	36.4	34.8	34.8	34.8	34.8
	Score	99	29	26	25	24	24	24	24	23	23	23	23
	Result No.	1	7	m	4	2	9	7	80	6	10	11	12

P. falciparum circ	Peptide from P.fal	from P	- 0	Peptide P5 Synt	n analog		5	motif	CO:		Synthetic peptide	-	Ø	Bovine aprotinin w	CENP-B protein amil	Peptide correspond	Membrane dipeptida	Plasmodium falcipa	HIV gag protein de		Yeast Smll C-termi	E.coll adventitial	H-CDR-3 of anti-id	۵	CAl pro	Inhibitor of TK of	Human hepatitis C	HSV specific antlg	T cell epitope/MHC	der i	Hydrophilic, acidi	. Hydroxymethylaluta
88		۰۰	99	W79734	R27122	P82670	W06267	W06269	R92853	W54540	W54541	W82749	W82750	W82751	R62208	R50265	Y48741	R87291	Y25216	W84220	Y90473	P82330	R74936	Y77821	Y77822	R44862	R62589	Y13405	Y10214	W24966	R62118	W21259
					13	σ			17	13	19	70	20	70	15	15	20	16	20	20	21	6	16	21	21	14	16	20	20	18	15	16
80	æ	80	8							13					9	7	ω	σ	σ	6	6		10								7	7
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34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	m	3	33	33	31	3
23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	21	21
13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

R90945 standard; peptide; 13 AA. (first entry) 09-SEP-1996 RESULT R90945

Factor VIII antigenic peptide corresp. to residues Arg1652-Tyr1664.

Factor VIII; modification; inhibitor activity; binding; antibody; von Willebrand factor; immune disorder.

Synthetic.

95WO-BE00068. 94BE-0000666. WO9602572-A2. 14-JUL-1995; 14-JUL-1994; 01-FEB-1996.

(CROI-) CROIX ROUGE BELGIQUE. Laub R; WPI; 1996-105861/11. Di Giambattista M,

Factor VIII antigenic polypeptide fragments and epitope(s) - also inhibitors of factor VIII and anti-inhibitors, useful for e.g. preventing and treating immune disorders involving inhibition of factor VIII binding

my hid When

Claim 8; Page 30; 45pp; French.

Length 13;

Query Match

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ó
                              modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to von Willebrand factor, esp. antibodies, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The synthetic peptide has a sequence based on regions of homology between Bordetella pertussis toxin S-subunits. The peptide acts as an analogue of the selectins ELAM, GMP140 and hLHR. Antibodies to this peptide can block the function of selectins and prevent the adherence of circulating cells to endothelial cells and inhibit inflammatory, metastatic or coagulation processes. The peptide also functions as a carrier to direct selected therapeutic agents to cells bearing selectin-specific receptors such as leukocytes, platelets or high endothelial veniles. The antibodies will further prevent binding of B. pertussis to eukaryotic cells such as ciliated cells and macrophages to interfere with the persistence of B. pervent binding of a host. In addition, the peptide can function as a vaccine to protect against B. pertussis infection.
               Peptides R90945-64 are derived from the factor VIII protein, esp. from a
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide(s) inhibiting adhesion between circulating cells and endothelia - contain sequences homologous to Bordetella pertussis and selectins 1, used for treating malignancy or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHR; pertussis toxin; PT; GMP140; metastasis; coagulation;
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                                                                                                                                                                                Length 13;
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0
                                                                                                                                                                                               Pred. No. 6.4e-06;
                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caused by infection or auto:immune disease
                                                                                                                                                                                100.0%; Score 66;
100.0%; Pred. No. 6
                                                                                               preventing or treating immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selectin based anti-adhesion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 52; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                             R28967 standard; peptide; 13 AA.
                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0695532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US03701
                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1993 (first entry)
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuomanen E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation; vaccine.
                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                               1 RTTLQSDQEEIDY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-398798/48.
                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9219646-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1992.
                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masure HR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                             R28967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELAM;
                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W06255-W06276 are immunoreceptor tyrosine-inhibitory motifs (ITIMs) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bind to protein tyrosine phosphatase IC (PTPID), PTPID, p160 or PTO and in doing so, inhibit signal transduction pathways involving these molecules. ITIM motif containing peptides can be used for regulating inflammatory and immune responses and for drug screening. The peptides can also be used to regulate haematopoietic cell function, especially antibody responses, blood clotting initiation, inflammatory responses, release of cytokines or mediators, or cytotoxicity and are useful for treating an immunoproliferative, immunodeficiency, autoimmune or infectious disease, cancer or allergic response. The peptides can also be used in the production of antibodies and in assays and diagnostics.
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immuno-receptor tyrosine-inhibitory motif peptide(s) - used to develop methods for regulating inflammatory and immune responses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                   ITIM; immunoreceptor tyrosine inhibitory motif; haematopoiesis; blood; clotting; antibody response; inflammation; cytokine release; immunoproliferative; immunodeficiency; autoimmune; infectious; disease; cancer; allergy; drug screening.
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                             ITIM motif used to regulate haematopoietic cell function.
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "preferably non-hydrolysable
                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphotyrosine analogue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
DB 13;
29;
                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                    W06271 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 88; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
43.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US02289
                                                                                                                                                                                                                                (first entry)
               Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                         1 tvlaiqneeiey 12
                                                            2 TTLQSDQEEIDY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-412740/41.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9626961-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1996.
                                                                                                                                                                                                                               15-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambier JC;
                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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W06271
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QSDQEEIDY 13

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13 AA;

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 DQEEID 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|:||
4 dkedid 9
                                                                                                            10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
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        WO9904265-A2
                                                    15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1999
                                                                                      17-JUL-1997;
10-OCT-1997;
                               28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X07131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer
breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               The protein fragment was isolated for comparison with the rotavirus segment 8 protein fragment isolated from the Hu/Australia/5/11. The segment 8 product and fragments comprise at least part of the major outer capsid glycoprotein, they may be expressed from a transformed host and are useful as antigens for vaccination and diagnosis of the rotavirus.
                                                                                                                                                                                                                                                                                                                                                                              RNA gene segment coding for outer capsid glyco:protein of rota:virus - useful in expression of antigenic viral proteins by bacteria for use in vaccines and diagnostic prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                      Fragment of SAll rotavirus major outer shell glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 7; Length 12; Pred. No. 1.4e+02; 1; Mismatches 3; Indels
                                                                                                                                              Hu/Australia/5/77 rotavirus; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y07173 standard; Peptide; 10 AA.
                                                   P60552 standard; Protein; 12 AA.
                                                                                                                                                                                                                                                            84AU-0004733.
85WO-AU00096.
85AU-0042970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%;
55.6%;
                                                                                                                                                                                                                                       85WO-AU00096
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                            (UYME-) UNIV OF MELBOURNE.
                                                                                                                                                                                                                                                                                                                                 Dyall-Smith ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.ه
در 5: Conservative
                                                                                                                                                                   SAll simian rotavirus.
                                                                                                                                                                                                                                                                                                                                                       WPI; 1986-028178/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TLQSDQEEI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1999
                                                                                                                                                                                                                                       29-APR-1985;
                                                                                                                                                                                                                                                              27-APR-1984;
                                                                                                                                                                                                                                                                         29-APR-1985;
01-JAN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                 24-JUN-1991
                                                                                                                                                                                                                21-NOV-1985
                                                                                                                                                                                          WO8505122-A
                                                                                                                                                                                                                                                                                                                                  Holmes I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y07173;
                                                                          P60552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                              RESULT
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antiguals. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, remal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated antigen; diagnosis; research; treatment; human; cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated cancer associated nucleic acids and polypeprides - isolated using sera from cancer patients, used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Pred. No. 1.7e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                               Stockert E;
                                                                                                                                                                                                                                                                                                                                                                               Obata Y,
                                                                                                                                                                                                                                                                                                                                                                                                               Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 16; Page 763; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                           O'Hare M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y07131 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                            97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.4%;
66.7%;
98WO-US14679
                                                                98US-0102322
                                                                                                                                                                                                                                                                                                                                                                    Chen Y, Gout I, Gure A,
Pfreundschuh M, Sahin U,
Tureci O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-132448/11.
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Query Match
Best Local Similarity
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                                                                           WPI; 1995-293118/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-418755/35.
                                                                                                                                                                                                                                                                                                           AA;
                                (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                    7 DQEEIDY 13
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2 deqdtdy 8
                                                                                       N-PSDB; T03910
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           14-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9931134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silverman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1999.
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y27136;
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product to a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                        The invention relates to a method for diagnosing a disorder characterised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD45; immune system; disease; pp32; T-lymphocyte; T-cell; activation; isoform; CD2; phorbol ester; identification; screening; monoclonal antibody.
                                                                                                                                                                                                         New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 20; Length 10;
Pred. No. 1.7e+02;
2; Mismatches 0; Indels
                                                                                                                                         old LJ;
                                                                                                                                        O'Hare M, Obata Y, Old
Scanlan MJ, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V8 fragment of CD45 associating protein pp32.
                                                                                                                                                                                                                                                    Example 16; Page 756; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R82679 standard; Protein; 11 AA.
                                                                                                                     (LUDW-) LUDWIG INST CANCER RES.
                                        98US-0102322.
97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.4%;
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                    98WO-US14679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                          Gure A,
Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                    WPI; 1999-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                      Gout I,
                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA;
                                                                                                                                                     Pfreundschuh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 DQEEID 12
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4 dkedid 9
                                                  17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
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                     15-JUL-1998;
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28-JAN-1999
                                         22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-1995
                                                                                                                                                              Tureci O;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                         Chen Y,
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Hmunc13; glucose-regulated; kidney; renal; microvascular; hyperglycemia; diabetes mellitus; apoptosis; vesicle trafficking; glomerulopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pp32 is specifically associated with, and is a potential substrate or CD45. pp32 is constitutively phosphorylated on serine in resting recels. In such cells it exists in two isoforms, pp32 low and pp32 high. Both isoforms show rapid changes during T-cell activation. These changes take place within five minutes after stimulation of T-lymphocytes with monoclonal antibodies specific for CD2 or with phorbol esters. pp32 is useful for treating diseases of the immune system and to identify inhibitors of T-cell activation. Peptide fragments of pp32 (RB5073-81) were used to produce degenerate primers (T03911-19) which were then used to produce a probe to isolate a full length pp32 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding a human pp32 protein which associates with CD45 - useful for treatment of immune system diseases and in the identification of T cell activation inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 16; Length 11., Pred. No. 1.9e+02;
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                                                                                                                                               Schoenhaut D, Schraven B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Page 25; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y27136 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.4%;
94US-0197793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0069352.
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                                                                                                                                           Meuer S, Ratnofsky S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             renal failure; human.
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Gaps

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Length 7; Indels

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Blocker; inhibitor; T-cell; T-helper cell; DR3; autoimmune diamate; type 1 diabetes; immunosuppression; Grave's disease; Sjorgens syndrome; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides (R46052-6057) are specific examples of a generic formula. The peptides prevent the activation of salf-reactive T helper calls which lead to the destruction of "self" calls and tissues. The peptides bind to a particular HLA-DR molecule but are not recognised by the self-reactive T helper cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide(s) which block self reactive helper T cells restricted to DR3, for treating or preventing autoimmune diseases, e.g., type I diabetes, without causing generalised immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 57.1%; Pred. No. 2.1e+05; 4; Conservative 2; Mismarrhan
                                             Score 23; DB 15; Le
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                    DR3-restricted T-helper cell blocking peptide.
                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ottenhoff THM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 25; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R43245 standard; peptide; 8 AA.
                                                                                                                                                                                                                               R46057 standard; peptide; 7 AA.
                                                          h 34.8%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-NL00151.
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                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geluk A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-048794/06.
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Matches 4; Conserv
                                                             Query Match
Best Local Similarity
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                 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TLQSDQE 9
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1 tigydee 7
                                                                                                                       3 TLQSDQE 9
                                                                                                                                          1: ||:|
1 tiasdee 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUL-1993;
                                                                                                                                                                                                                                                                                          26-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9402509-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                  Sequence
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                                                                                                                                                                                                 RESULT 10
                                                                                           Matches
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                                        The invention provides a human glucose-regulated munc protein, Hmuncl3, isolated from kidney. Host cells transformed with a vector comprising the Hmuncl3 gene are used for the recombinant expression of the protein. The Hmuncl3 gene is regulated by glucose. Hmuncl3 contributes to the renal and microvascular complications associated with hyperglycemia in diabetes mellitus. Hmuncl3 is used for apoptosis or vesicle trafficking. Hmuncl3, its gene or Hmuncl3 specific antibodies can be used in a kit for the Such disorders include insulin dependent and independent diabetes mellitus, glomerulopathy and (ischaemic) renal failure. A method using inhibitors (preferably an antisense nucleotide sequence Hmuncl3 gene) or activators of Hmuncl3 activity or its expression are useful in the treatment or detection of the above diseases. The present sequence treatment of the above diseases. The present sequence
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blocker; inhibitor; T-cell; T-helper cell; DR3; autoimmune disease; type 1 diabetes; immunosuppression; Grave's disease; Sjorgens syndrome; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides (R46052-6057) are specific examples of a generic formula. The peptides prevent the activation of self-reactive T helper cells which lead to the destruction of "self" cells and tissues. The peptides bind to a particular HLA-DR molecule but are not recognised by the self-reactive T helper cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide(s) which block self reactive helper T cells restricted to DR3, for treating or preventing autoimmune diseases, e.g., type I diabetes, without causing generalised immunosuppression
                                                                                                                                                                                                                                                                                                                                    36.4%; Score 24; DB 20; Length 13; 62.5%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR3-restricted T-helper cell blocking peptide.
                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                             specific polyclonal antibody was prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ottenhoff THM;
              Disclosure; Page 25; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 25; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R46053 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devries RRP, Geluk A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-048794/06.
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                        13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  2 TTLQSDQE 9
                                                                                                                                                                                                                                                                                                                                                                                                                              1 tirqsdee 8
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                                                                                                                                                                                                                                                                                           Sequence
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R46053
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Gaps

Elvin J,

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The sequence is that of peptide cp29 which is recognised by, or can induce, cytotoxic I lymphocytes. It may be useful in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Circumsp. 368-375; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte; viruses; parasites; tumours; antigens; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A compsn. which induces a cytotoxic T lymphocyte (CTL) response to an antigen (Ag) in a mammal comprises, a CTL Ag response inducing peptide (L.e. R78824-R78853) and a lipid conjugated helper T cellinducing peptide. The compsn. induces a CTL response to bacterial, viral or tumour Ags, and is therefore useful in the treatment and prevention of diseases associated with the Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compsn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment and prevention of diseases associated with the antigen e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P. falciparum circumsp. 368-375 cytotoxic T lymphocyte epitope.
                                          Peptide(s) recognising or inducing cytotoxic T lymphocytes useful in vaccines against malaria or HIV-2, derived from specific antigen and human leukocyte antigen contg. class I
                                                                                                                                                                                                                                                                       Length 8;
                                                                                                                                                                                                                                                                    Score 23; DB 14; Length 8;
Pred. No. 2.1e+05;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitiello MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17; 109pp; English.
                                                                                                                           Claim 6; Page 30; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            R78840 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                     34.8%;
50.0%;
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                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
              WPI; 1993-336833/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-302545/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease prevention.
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CYTE-) CYTEL CORP.
                                                                                             restricted epitope
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                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                  8 QEEIDY 13
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3 kdeldy
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                                                                                                                                                                                                                         Seguence
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                                                                                                                                                                                          malaria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R78840;
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                             R78840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of peptide cp26 which is recognised by, or can induce, cytotoxic T lymphocytes. It may be useful in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                             Peptide(s) recognising or inducing cytotoxic I lymphocytes - useful in vaccines against malaria or HIV-2, derived from specific antigen and human leukocyte antigen contg. class I restricted epitope
                                                                                                                                                                                                                                                                                                                Whittle HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gotch FM, Hill AV, McMichael AJ, Whittle HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                          Cytotoxic T lymphocyte recognition/induction peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytotoxic T lymphocyte recognition/induction peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 14; L. Pred. No. 2.1e+05; 3; Mismatches 0;
                                                                          CTL; vaccine; malaria; specific antigen-derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTL; vaccine; malaria; specific antigen-derived
                                                                                                                                                                                                                                                                                                                  McMichael AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 30; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R43246 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                  Gotch FM, Hill AV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.8%;
50.0%;
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                                                                                                                                                                                                                                                                                 (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                     93WO-GB00711
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92GB-0017704
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             (first entry)
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Best Local Similarity 50.0v
Pest Local 3; Conservative
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                                                                                                                                                                                                     05-APR-1993;
                                                                                                                                                                                                                                   03-APR-1992;
20-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-1992;
20-AUG-1992;
             04-MAY-1994
                                                                                                                                       WO9320103-A
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3 kdeldy
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                                                                                                                                                                      14-OCT-1993
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                                                                                                         Synthetic.
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Sequence malaria.

R43246;

RESULT 12 R43246

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Elvin J,

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The peptides W54559-W54809 are examples of peptides to which at least I (preferably 2) mannose can be attached to increase their uptake as antigens by antigen-presenting cells. Uptake of agonist mannosylated peptides will increase the T cell response, whereas uptake of antagonist peptides blocks the T cell response. Blocking binding of immunogenic autoantigens can be used in treatment of type I diabetes, rheumatoid arthritis, graft rejection etc., also to induce T-cell non-responsiveness. Vaccines containing mannosylated antigen are used to prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths and parasites.
                                                                                                                                                  Mannose; antigen; antigen-presenting cell; mannosylated peptide; {\tt T} cell; vaccine; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing uptake and presentation of antigen(s) - by adding mannose residue(s) to antigen for increasing T cell response, useful in, e.g. vaccines against viral infection(s)
                                                                            Peptide from P. falciparum CSP 368-375 b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 29; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-NL00536.
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          25-SEP-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koning F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-230631/20
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Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|:||
3 kdeldy 8
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                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The peptides w54559-w54809 are examples of peptides to which at least 1 (preferably 2) mannose can be attached to increase their uptake as antigens by antigen-presenting cells. Uptake of agonist mannosylated peptides will increase the T cell response, whereas uptake of antagonist peptides blocks the T cell response. Blocking binding of immunogenic autoantigens can be used in treatment of type I diabetes, rheumatoid arthritis, graft rejection etc., also to induce T-cell non-responsiveness. Vaccines containing mannosylated antigen are used to prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths and parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen; antigen-presenting cell; mannosylated peptide; T cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing uptake and presentation of antigen(s) - by adding mannose residue(s) to antigen for increasing T cell response, useful in, e.g. vaccines against viral infection(s)
                                                                                    Gaps
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       Score 23; DB 16; Length 8; Pred. No. 2.1e+05; 3; Mismatches 0; Indels
                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide from P.falciparum CSP 368-375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 29; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                           W54663 standard; peptide; 8 AA.
       34.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-NL00536
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                                                                            3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drijfhout JW, Koning F;
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Ouery Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W54663;
                                                                                                                                                                                                                                                                                                                          RESULT 14
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Search completed: January 17, 2001, 13:34:23
Job time: 543 sec
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Gaps

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Indels

Conservative

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Best_Local Similarity Matches 3; Conser 8 QEEIDY 13 W54664 standard; peptide; 8 AA.

15

RESULT W54664 W54664

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Score 23; DB 19; Length 8; Pred. No. 2.1e+05; 3; Mismatches 0; Indels

34.8%; 50.0%;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:31:20 ; Search time 13.67 Seconds (without alignments) 64.573 Million cell updates/sec Run on:

US-08-765-837-1 66 1 RTTLQSDQEEIDY 13 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues Searched:

1828 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		prote		hemocyanin subunit	d prot	t ston	H-a -	ome P4	beta-conglycinin a	T-cell receptor be	ien rec	.n, fas	- 66000	protein	3.4	coxida	1.4K	<u>-</u>	V-D-J r	7-D-J r	soybean	1A - S	len rec	deoxynucleotidyltr	chain	chain CRD	leucosulfakinin-II	3.4.22	itin -	nin II
	ption	hypothetical	n alph	anins	wound-induced	urinary tract	glycoprotein H	NADP-cytochrome	onglyc	recep	antigen	calsequestrin,	protein QA300039	1-69 p	hementin (EC	cytochrome-c	hypothetical	hypothetical	chain \	chain V-D-J	ı	equinatoxin	antiqen	ucleot	vicilin 72K chain		ulfaki	n (EC 3	bacterioferritin	leucosulfakinin
	Description	hypoth	tubuli	hemocy	-punom	urinar	glycop	NADP-C	beta-c	T-cell	T-cell	calsed	protei	late G1-69	hement	cytoch	hypoth	hypoth	Ig H C	Ig H c	actin 7	eduina	T-cell	deoxyn	vicili	Ig heavy	leucos	calpain	bacter	leucos
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		T46862	S65612	н61308	9775	B56049	A40795	S18385	6335	51737	S47371	B39040	PA0035	PH0108	A61007	S43625	JQ2308	JQ2318	PH1605	PH1611	S15755	PC1149	S47373	49637	A34818	PT0299	GMROL2	39392	182	959
	ID	T46	S65	H61	S19	B56	A40	S18	S16	S51	S47	B39	PAO	PH0	A61	S43	302	302	PH1	PH1	S15	PC1	S47	149	A34	PTO	GMR	839	S48	B606
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æ	Query Match 1	30.3	30.3	28.8	28.8	28.8	27.3	27.3	27.3	•	•		-	25.8	•	25.8	-	25.8	٠	25.8	δ.	'n.	ď.	δ.	24.2	•		24.2	24.2	24.2
	Score	20	20	19	19	19	18	18	18	18	18	17	17	17	17	17	17	17	17	17	17	17	17	17	16	16	16	16	16	16
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kassinin - Senegal Ig H Chain V-D-J r	tubulin beta chain	spore proteinase q	tram protein - Esc	hypothetical prote	cerebellar degener	triacylglycerol Li	dissimilatory sulf	neuropeptide - flo	cytochrome-c oxida	alpha-amylise (EC	T-cell receptor be	quinoline 2-oxidor	chemical-sense-rel	cytochrome-c oxida
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30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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hypothetical protein algT [imported] - Pseudomonas aeruginosa (frugment)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Tymar-2000 #text_change 21-Jul-2000
C;Accession: T46862
R;DeVries, C.A.; Hassett, D.J.; Flynn, J.L.; Ohman, D.E.
Gene 156, 63-67, 1995
A;Title: Genetic linkage in Pseudomonas aeruginosa of algT and nadB: mutation in nadB
A;Reference number: Z24110; MUID:9525569
A;Accession: T46862
A;Ac

0; Gaps Length 13; Score 20; DB 2; Length 13; Pred. No. 1.3e+03; 4; Mismatches 3; Indels Query Match 30.3%; Best Local Similarity 30.0%; Matches 3; Conservative 6

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3 TQEQDQQLVE 12 3 TLQSDQEEID 12 ŏ

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C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Species: Boot-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C.Species: Boot-1865612
R.Ruediger, M.; Plessmann, U.; Ruediger, A.H.; Weber, K.
FEBS Lett. 364, 147-151, 1995
A;Fitle: Beta tubulin of bull sperm is polyglycylated.
A;Reference number: 865611; MUID:95269788
A;Reference number: 856611; MUID:95269788
A;Accession: 855612
A;Accession: 865612
A;Molecule type: protein
A;Residues: 1-13 <RUE>

Gaps ; 0 30.3%; Score 20; DB 2; Length 13; 50.0%; Pred. No. 1.3e+03; Live 2; Mismatches 1; Indels Query Match 30.3 Best Local Similarity 50.0 Matches 3; Conservative

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Glycoprotein H-a - bovine (fragment)
Clypecies: Bos primigenius taurus (cattle)
Clypecies: Bos primigenius taurus (cattle)
Clypecies: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 31-Dec-1993
Clypecossion: A40795
R;Christie, D.L.; Batchelor, D.C.; Palmer, D.J.
J. Biol. Chem. 266, 15679-15683, 1991
A;Title: Identification of kex2-related proteases in chromattiu granutes by partial a A;Reference number: A40795
A;Accession: A40795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 07-Feb-1997 :
C;Accession: S18385
R;Nadler, S.G.; Strobel, H.W.
Arch. Biochem. Blochem. Blochem. Blochem. Blochem. A;Tille: Identification and characterization of an NADPH-cytochrome P450 reductase de A;Reference number: S18385; MUID:92027739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
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C;Date: 21-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S16335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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NADP-cytochrome P450 reductase-related protein - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 2; Length 11;
Pred. No. 2.5e+03;
Tred. no. 2.5e+03;
Tred. no. 2.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 2; Length 1T;
Pred. No. 2.5e+03;
0; Mismatches ' 2; Indels
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A;Title: Characterization of the subunits of beta-conglycinin. A;Reference number: S16334; MUID:86049421
A;Accession: S16335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S16335
beta-conglycinin alpha chain soybean (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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66.78;
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Matches 4; Conservative
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Matches 3; Conservative
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A; Residues: 1-11 < CHR>
C; Keywords: glycoprotein
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A, Residues: 1-11 <NAD>
C, Keywords: NADP
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A, Molecule type: protein
A, Residues: 1-12 <COA>
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SDQEE 10
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1 NDQEQ 5
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                                                                                                                 hemocyanin subunit IV - Atlantic horseshoe crab (fragment)
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 17-Jul-1994 #Sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: H61308
R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
R;Jolles, J.; Jolles, Jolles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BIN>
A:Experimental source: urate-calcium oxalate kidney stones
A:Experimental source is designated as Homo sapiens, however the true source probably origi
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C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 20-Apr-2000
C;Accession: B56049
R;Binette, J.P.; Binette, M.B.
Scanning Microsc. 8, 233-239, 1994
A;Title: Sequencing of proteins extracted from stones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
C;Accession: S19775
R;Parsons, B.L.
B;Reference number: S19773
A;Reference number: S19773
A;Reference number: S19773
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Pred. No. 1.5e+03;
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Pred. No. 1.6e+03; 
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-11 <PAR>
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wound-induced protein - tomato (fragment)
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ilarity 37.5%;
Conservative
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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Gaps

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Indels

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C;Accession: A61007
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 359-369, 1990
A;Tithe: Purification and characterization of hementin, a fibrinoqenolytic proteuse t
                                                                                                                                                                                                                                                                                                                                          C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C; Accession: PA0012 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C; Accession: PA002 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
R; Kamo, M: Kawakami, T.; Miyatake, N.; Tsugita, A.
S; Damitted to JIPID, July 1994
A; Deference number: PA0001
A; Reference number: PA0001
A; Reference number: PA0001
A; Residues: 1-8 < KAM>A; Residues: 1-8 < KAM>A; Experimental source: stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Haementeria ghilianii (Amazon leech)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-Muy-1999
                                                                                                  Length 7;
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                                                                                                Score 17; DB 2;
Pred. No. 2e+05;
3; Mismatches (
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Pred. No. 2e+05;
2; Mismatches
                                                                                                                                                                                                                                                                                                                         protein QA300039 - Arabidopsis thaliana (fragment)
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  A;Molecule type: protein
A;Residues: 1-7 <CAL>
C;Keywords: phosphoprotein; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      late G1-69 protein - mouse (fragment)
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Best Local Similarity 40.0°
Matches 2; Conservative
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Best Local Similarity 33.3
Matches 3; Conservative
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Matches 3; Conservative
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1 EGDDEGEEY
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2 DEEDL 6
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PH0108
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: B39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein A;Reference number: A39040; MUID:91093153
A;Accession: B39040
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A;Reference number: S47355
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C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell antigen receptor VJ junction beta chain - human C;Species: Homo sapiens (man) C;Date: 06.Jan.1995 #sequence_revision 06.Jan.1995 #text_change 05-Nov-1999 C;Accession: S47371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Accession: S47371
A.Status: preliminary
A.Molecule 'type: mRNA
A.Residues: 1-13 < LEH>
A.Residues: 1-13 < LEH>
C.Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNÅ
A;Residues: 1-12 FOUR>
A;Cross-references: EMBL:228345; NID:g607126; PIDN:CAA82199.1; PID:g607127
C;Keywords: T-cell receptor
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R;Purinovic:Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S51732
A;Accession: S51737
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 2; Length 12; Pred. No. 2.7e+03; 3; Indels
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                     Indels
Pred. No. 2.7e+03;
; Mismatches 2;
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Pred. No. 3e+03;
4; Mismatches
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Best Local Similarity 37.5
Matches 3; Conservative
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Best Local Similarity 37.5
Matches 3; Conservative
                     Conservative
Best Local Similarity
Matches 2; Conserv
                                                          LQSDQEEID 12
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1 VEEEEEEXE 9
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Oytochrome-c oxidase (BC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)
C.Species: Oncorhynchus mykiss (rainbow trout)
C.Species: Oncorhynchus mykiss (rainbow trout)
C.Species: Ooct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C.Accession: 543625
B.F.Feund, R.; Kadenbach, B.
Eur. J. Blochem. 221, 1111-1116, 1994
A.F.Itle: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrd A.Reference number: 543624; MUID: 94237150
A.Accession: 543625
A.Molecule type: protein
A.Residues: 1-10 cFRE>
A.Note: the source is designated as Salmo gairdneri
C.Genetics: 1-10 cFRE>
A.Note: the source is membrane-associated complex; mitochondrion; oxidoreductase
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A;Reference number: A61007; MUID:90256973
A;Accession: A61007
A;Wolecule type: protein
A;Residues: 1-10 <SWA>
C;Keywords: anticoagulant; hydrolase; saliva
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1 TTLTEPEPDL 10
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Search completed: January 17, 2001, 13:34:57 Job time: 217 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:34:25 ; Search time 8.41 Seconds (without alignments) 49:920 Million cell updates/sec Run on:

US-08-765-837-1 66 1 RTTLQSDQEEIDY 13 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

88757 seqs, 32294092 residues Searched:

518 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q46464 campylobact			P15987 glycine max		P38641 mus musculu	P30087 homo sapien	P09039 leucophaea	_		P13973 escherichia	P56576 rattus norv		P21144 leucophaea		P80464 comamonas t	Q05055 tetrahymena	P81411 porphyromon	P14537 ceratotheri	P11180 bos taurus		_	P47733 locusta mig	P30369 macropus eu				4	C)	-	4 litoria	ب	P80677 chelyosoma
SUMMARIES	ID	SYK_CAMUP	UCRH_MOUSE	COXA_ONCMY	ACT7_SOYBN	ORCK_ORCLI	UF03_MOUSE	UPA1_HUMAN	LSK2_LEUMA	COXA_CANFA	TKN_KASSE	TRM3_ECOLI	UH11_RAT	COXG_RAT	LCMS_LEUMA	SPI_HALRO	Q2OA_COMTE	CALM_TETTH	LPAA_PORGI	FIBB_CERSI	ODP2_BOVIN	UPA9_HUMAN	VEG6_BACSU	LOSK_LOCMI	CCKN_MACEU	FAR1_CALVO	FIBB_ERYPA	FLA2_TREHY	LPCA_STAAU	NSK1_SARBU	UF02_MOUSE			GON1_CHEPR
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	Result No.	Н	7	m	4	2	9	7	80	σ	10	11		13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	50	30	31	32	33

p41494 drosophila p55556 caenorhabdi p81672 pinus pinas p04428 leucophaea p31688 periplaneta p3164 homo sapien p41478 oryctolagus p43669 salmonella p54712 canis famil p81345 clostridium p25423 melolontha
NEMS_DROME UP11_CAEEL HS70_PINPS LSK7_DENPS LSKP_PERAM UKA2_HUMAN FIBB_RABIT PRC_SALTY SODM_CANFA UN10_CLOPA AKH_MELML
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199.7 199.7 199.7 199.7 199.7 199.7 199.7 199.7
122
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ALIGNMENTS

J Q I	SYK_CAMUP STANDARD; PRT; 10 AA.
8 E E	046464; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last semience undate)
1 1 1	(Rel. 37,
E E E	
SO	Campvlobacter upsaliensis,
88	Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
88	Campylobacter.
Z Z	SECTIONCE FROM N.A.
RG.	
ZZ a	PubMed=8996110;
R R	bourke b., kasnid s.T., Bingnam H.L., Chan V.L.; "Characterization of Campvlobacter upsallensis fur and its
RT	localization in a highly conserved region of the Campylobacter
RT	genome.";
RL 20	
္ဗင္	-!- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) = AMP + PVROBHOSDHATE + L-LYSYL-TRNA/LYS\
ვ <u>ც</u>	-I- SUBDIT: HOMODIMER (BY SIMILARITY).
ပ္ပ	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
ပ္ပ	-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
י כ	
	This SWISS-PROT entry is copyright. It is produced through a collaboration
	Detween the Swits institute of Bioinformatics and the EMBL outstation -
ז כ	the European Blointolmarics instructe. There are no factorized on the
ខ	use by non-protit institutions as rough as its content is in way modified and this statement is not removed. Usage by and for commercial
U	entities requires a license agreement (See http://www.lsb-slb.ch/announce/
ຍ	or send an email to license@isb-sib.ch).
ပ္ပ	DMDT . 177076. AND41242 1
X 2	INTERPROTION CONTRACTOR
DR.	PROSTITE: PSON179: AA TRNA LIGASE II 1: PARTIAL.
DR	PROSITE; PS00339; AA TRNA LIGASE II 2; PARTIAL.
KK	Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
I OS	NON_TER 1 1 1 SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;
è	01 00000 00 00
E B K	edety match Best Local Similarity 33.3%; Pred. No. 6.8e+02; Matches 3. Conservative Mismatches 7. Indels 0. Cans 0.
2	s) conservative 4) mismacones 2) inders 0, caps

3; Conservative :: |: |:| 2 KSELKEDKE 10 1 RTTLQSDQE 9 Matches ò g

RESULT 2 UCRH_MOUSE

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PIR; S43625; S43625.
                                                                                                                                                                                                                                                                                                      ACTIN 7 (FRAGMENT).
                                                                                 Query Match
Best Local Similarity
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Matches 3; Conserv
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5 VETDEE 10
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P15987:
                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                       (CYTOCHROME B, CYTOCHROME CI, RIESKE PROTEIN), 2 CORE PROTEINS AND 6 LOW-MOLECULAR WEIGHT PROTEINS.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
Welgulinol-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN (EC 1.10.2.2)
(MITOCHONDRIAL HINGE PROTEIN) (CYTOCHROME C1, NONHEME 11 KDA PROTEIN)
(COMPLEX III SUBUNIT VIII) (FRAGMENT).
                                                                                                                                                                                                                                            SUBMITTED (AUG-1998) to the SWISS-PROT data bank.
-!- FUNCTION: THIS IS A COMPONENT OF THE UBTQUINOL-CYTOCHROME C
-REDUCTASE COMPLEX (COMPLEX III OF CYTOCHROME B-CI COMPLEX), WHICH
IS PART OF THE MITCCHONBIAL RESPIRATORY CHAIN. THIS PROTEIN MAY
MEDIATE FORMATION OF THE COMPLEX BETWEEN CYTOCHROMES C AND C1.
                                                                                                                                                                                                                                                                                                                -i- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2 FERROCYTOCHROME C. -i- SUBUNIT: BC1 COMPLEX CONTAINS 11 SUBUNITS; 3 RESPIRATORY SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 221:1111-1116(1994).
-!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
4 FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-2DPAGE; P99028; MOUSE.
Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94237150; PubMed=8181469;
Freund R., Kadenbach B.;
"Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
CYTOGHROME COXIDASE POLYPEPTIDE VA (EC 1.9.3.1) (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
BURATYOLA: Metzaca, Chordatta, Craniata, Veritebratta, Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygiis Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .: - SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
                                                                                                                                                                                                        Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X., Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 1; Lengtn 12;
Pred. No. 1.2e+03;
. --t-hes 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6B256F18801B1B1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE UQCRH/QCR6 FAMILY
 12 AA
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 PRT;
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28.6%;
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ::||:
EEEEEEL 11
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                                                                                                                                                                                          TISSUE-LIVER;
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 UCRH_MOUSE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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IN VARIOUS TYPES OF CELLE.
IN VARIOUS TYPES OF CELLE.
-- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN INPORTANT ROLE IN CYTOPLASMING, CELL CHAPE DETERMINATION, CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
-- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Diverse soybean actin transcripts contain a large intron in the 5' untranslated leader: structural similarity to vertebrate muscle actin
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max (Soybean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Magnoliophyta; eudicotyledons; core eudicots; Rosidae; curosids I;
Fabales; Fabaceae; Papilionoldeae; Glycine.
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0
                                                                                                                  Score 17; DB 1; Length 10;
Pred. No. 1.5e+03;
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                                                         C535C5B1AB02C33D CRC64;
Oxidoreductase; Heme; Mitochondrion; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8BEFF3C36D4FD05A CRC64;
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Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AA
                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. WAYNE;
MEDLINE-91346640; PubMed-2102831;
Pearson L., Meagher R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes.";
Plant Mol. Biol. 14:513-526(1990).
                                                                                                                                           25.8%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X17120; CAA34980.1; -.
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50.0%;
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                                                      10 AA; 1144 MW;
                                                                                                                                                                                                    2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                              2
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RESULT 5 ORCK_ORCLI S

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"Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.9, ITS MW IS: 65 KDA.
                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost.oml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-L.MADERAE;
MEDLINE-87048769; PubMed-3778455;
Machman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
Nachman R.S., Holman B.D., Bolocked sulfated insect neuropeptide with homology to chholecystokinin and gastrin.";
Biochem. Biophys. Res. Commun. 140:357-364(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Periplaneta americana (American cockróach).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaría,
                                                                                                                                                                                                    Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquall C., Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;
                                                                              UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                     24.2%; Score 16; DB 1; Length 8; 100.0%; Pred. No. 8.9e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        944 MW; C01772C455BB06DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
LeuCOSULFAKININ II (LSR-II)
LeuCOphaea maderae (Madeira cockroach), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-P.AMERICANA; TISSUE-CORPORA CARDIACA; MEDLINE-90137190; PubMed-2615921;
                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last Sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA.
    AA.
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   PRT;
                                                                                                                                                                           TISSUE-PLASMA;
MEDLINE-93092937; PubMed-1459097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
   STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A26335; GMROL2 PIR; B60656; B60656
                                                                                                                                                                                                                                                                                                                                                                                        8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Veenstra J.A.;
UPA1_HUMAN
P30087;
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P09039;
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SEQUENCE
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UNSURE
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                                                                                                                                                                                                                                                    MEDLINE=93126144; PUDMed=1480511; Stangler N.; Stangler J., Hilbich C., Burdik S., Keller R.; Corowinin: a novel myotropic peptide from the nervous system of the crayfish, Orconectes limosus."; Peptides 13:859-864(1992).
-!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND AMPLITUDE OF SPONTAMEDOS HINDGUT CONTRACTIONS.
-!- TISSUE SPECIFICITY: ABDOMINAL NERVE CORD AND HINDGUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-TEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P36) (FRAGMENT).
                                                                                                                                        Orconectes limosus (Spinycheek crayfish).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 1; Length 13;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 1; Length 7;
Pred. No. 8.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     8A318D7B4A93A40A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6AA72B1DDB1B1180 CRC64;
                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA.
                                              13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                          Astacoidea; Cambaridae; Orconectes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%;
75.0%;
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     13 AA; 1518 MW;
                                                                                                                                                                                                                                        TISSUE-ABDOMINAL NERVE CORD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 842 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                              STANDARD;
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide.
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3 DEID 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 EEID 12
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EEAELD
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P38641;
                                            ORCK_ORCLI
P37086;
                                                                                                                            ORCOKININ.
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RESULT 6 UF03_MOUSE

õ g PROSITE; PS00259; GASTRIN; 1.

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Gaps

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                               Experientia 33:857-858(1977).
-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDIATR=86227859; PubMed=2836369;
MEDIATR=86227859; PubMed v. Obtsubo B.;
Inamoto S., Yoshioka Y., Obts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid IncFII R100.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Anastasi A., Montecucchi P.C., Erspamer V., Visser J.; "Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide from the skin of the African frog Kassina senegalensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16; DB 1; Length 12;
Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15; DB 1; Length 5; Pred. No. 8.9e+04; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                         -:- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
PIN. 507206; S07206.
INTERPRO. 1PR002040; -.
PROSITE; PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Amidation; Amphibian skin.
MOD_RES 1.2 1.2 AMIDATION.
SEQUENCE 12 AA; 1336 MW; 91757AB89Db6DBB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA; 634 MW; 6B1B1AA443500000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRAM PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conjugation; Plasmid; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.2%;
75.0%;
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Similarity 40.0%;
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRM3_ECOLI
P13973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia.
                                                                                                                                                                                                                         MUSCLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QSDQ 8
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4 KSDQ 7
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SEQUENCE
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
-!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
--- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
HSC-2DPAGE; P99501; DOG.
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn M.J., Corbett J.M., Wheeler C.H.; "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
                             PYRROLIDONE CARBOXYLIC ACID.
SULFATATION (IN L.MADERAE, BUT NOT IN
P.AMERICANA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kassina senegalensis (Senegal running frog),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
                                                                                                                                                                                                                                                                          4;
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0
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VA (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Length 11;
Pred. No. 2.5e+03;
3; Mismatches 0; Indels
                                                                                                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                     9B4F5391E86B5AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Heme; Mitochondrion; Inner membrane.
                                                                                                                                                                                                                    Score 16; DB 1; Ler
Pred. No. 2.3e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA.
                                                                                                               AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE. MEDLINE=77246385; Pubmed=891753;
        Sulfatation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%;
40.0%;
                                                                                                                                                                                                                    24.2%;
55.6%;
                                                                                                          10
1255 MW;
                                                                                                                                                                                                                    Query Match 24.2
Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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        Amidation;
                                                                                                          10
10 AA;
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6 ETDEE 10
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P08611;
        Hormone; 1
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
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Gaps

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RESULT 10 TKN_KASSE

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8 QEEIDY 13
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1 QNXLDF 6
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LCMS_LEUMA
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                                δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95324529; PubMed-7601105; Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.; Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - FUNCTION: THIS PROTEIN MAY BE ONE OF THE HEME-BINDING SUBUNITS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                         Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                   UH11_RAT STANDARD; PRT; / AA.
P56576;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P11) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Greated)
U-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUT. J. BIOCHEM. 230:235-241(1995).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
                                                                                                                                                                                                                                                                                         Submitted (SEP-1998) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 8.5, ITS MW IS: 42 KDA.
UNSURE 2 2 OR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB 1; Length 8;
Pred. No. 8.9e+04;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           22.7%; Score 15; DB 1; Length 7; 50.0%; Pred. No. 8.9e+04; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Mitochondrion.
                                                                                                                                                                                                                                                  STRAIN-WISTAR; TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.7%;
Best Local Similarity 33.3%;
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.7
Best Local Similarity 50.0
Matches 3; Conservative
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P80430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                       UH11_RAT
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Comp. Biochem. Physiol. 114B:1-9(1996).
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"Isolation, primary structure and synthesis of leucomyosuppressin,
an insect neuropeptide that inhibits spontaneous contractions of the
cockroach hindgut.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HEMOLYMPH;
MEDLINE-96231313; PubMed-8759295;
Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
"Purification and characterization of a 58,000-ba proteinase inhibitor from the hemolymph of a solitary ascidian, Halocynthia
                                                                                                                                                                                                                                                                                                                                      Comp. Biochem. Physiol. 85C:329-333(1986).
-i- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH PROTODEUM (HINDGUT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberlidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15; DB 1; Length 10;
Pred. No. 3.4e+03;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i-SUBUNIT: MONOMER.
-i-SUBLIARITY: BELONGS TO THE SERPIN FAMILY.
INTERPRO; IPRO0215; -.
PROSITE; PS00284; SERPIN; PARTIAL.
SERPIn; Serine protease inhibitor; Glycoprotein; Plasma.
NON_TER 10 AA: 1104 MW; 4225C7381B187Aa3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SERINE PROTEINASE INHIBITOR (FRAGMENT).
Halocynthia roretzi (Sea squirt).
Eukaryota; Mactazoa; Chordata; Urochordata; Ascidiacea; Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION,
D3C45229D2C1EAB2 CRC64;
                P21144; P41497;
01-MAY-1991 (Rel. 18, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-NOY-1995 (Rel. 32, Last annotation update)
LEUCOMYOSUPPRESSIN (LMS) (LEM-MS).
Leucophaea maderae (Madeira cockroach).
10 AA.
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  PRT;
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20.0%;
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Best Local Similarity 20.0
Matches 1; Conservative
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MOD_RES 1 1 1
MOD_RES 10 10
SEQUENCE 10 AA; 1275 M
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STANDARD;
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1 QDVDH 5
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Q10997;
  LCMS_LEUMA
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Gaps

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22.7%; Score 15; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels

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5 QSDQEE 10 : | | | 1 2 KKDGEE 7

δy qq

Search completed: January 17, 2001, 13:35:49 Job time: 84 sec

Uddyk7 mus sp. mep 04760 accherichia 08200 triticum ac 082070 tridodococcus 09484 homo sapien P78484 homo sapien 09484 homo sapien 095782 spinacia or 05782 spinacia or 05784 spinacia or 05784 spinacia or 09789 fullum s 09759 serratia ma 09759 serratia ap 09760 serratia ap 09262 buchnera ap

744875112788448

09N0J8 001128 001128 050038 047601 031295 09ZEZ1 09R862 093P674 063047 P8Z098

09QVK7 047600 082070 09UGG9 P72279 09UK84 P78484 09TZK9 09TZK9 06TZK9 06TZK9 06TZK9 06TZK9 06TZK9

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024365 drosophila
042507 triticum ae
04627 homo sapien
004131 lycopersico
099wu0 mus musculu
09fqy5 bos taurus
09bru0 schizosacch
066874 feline cali
                                                               ; Search time 19.04 Seconds
(without alignments)
80.026 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            374700 seqs, 117207915 residues
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                                                                 January 17, 2001, 13:34:25
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Q9QWU0
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Gapop 10.0 , Gapext 0.5
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1: Sp_archea:*
2: sp_bacteria:*
3: sp_tung!:*
4: sp_human:*
5: sp_invertebrate:*
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Match Length
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Maximum DB seq length: 13
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ALIGNMENTS

10 AC 00	Q24365 O24365:	PRELIMINARY;	PRT;	13 AA.	-
	01-NOV-1996		Created)	,	
10 E	01-NOV-1996 01-OCT-2000	(TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 15, Last annotation update)	Last sequ	nence update) station update)	
	YPOTHETICAL	HYPOTHETICAL 1.5 KDA PROTEIN IN IMPL2 5' REGION.	N IN IMPL2	5' REGION.	
	rosophila m	Drosophila melanogaster (Fruit fly).	uit fly).		
	ukaryota; k	detazoa; Arthropo	oda; Trach	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
	terygota; N	Weoptera; Endopte	erygota; D	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorphia;	comorpha
S 00	Ephydroidea; Dro	Ephydroidea; Drosophilidae; Drosophila. NCBI TAVIDA7027.	Drosophil	G	•
	SECUENCE FROM N.A.	M N.A.			
RC SJ	STRAIN-CANTON-S;	N-S;			
	EDLINE=9413	MEDLINE=94139565; PubMed=8306886;	06886;		
_	arbe J.C.,	Garbe J.C., Yang E., Fristrom J.W.;	Om J.W.;		
	IMP-L2: an	essential secret	ted immuno	"IMP-L2: an essential secreted immunoglobulin family member implicated	implicate
	n neural an	nd ectodermal de	velopment	in neural and ectodermal development in Drosophila.";	
	evelopment	Development 119:1237-1250(1993).	993).		
	!- CAUTION:	: THREE SHORT OF	EN READING	-!- CAUTION: THREE SHORT OPEN READING FRAMES ARE FOUND IN IMPL2 MRWA	PL2 MRW
	LEADER F	REGION, THESE MA	Y BE TRANS	LATED AS PART OF THE CON	APLETE
	IMPLZ PROTEIN.	CIEIN.			
	MBL; L23066	EMBL; L23066; AAB59249.1; -			
	LYBASE; FBG	FLYBASE; FBGNUOULZ5/; IMPLZ.			••
SQ SI	Hypothetical protein. SEQUENCE 13 AA; 14	1 protein. 13 AA; 1486 MW;		DE445043D063A736 CRC64;	
Query Ma Best Loo	atch Sal Simi 5:	33.3%; ilarity 55.6%; Conservative	Score 22; DB Pred. No. 1.3	DB 5; Length 13; 1.3e+03; Indels	
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Qy	5 QSDQEEIDY	IDY 13			
Db	3 QSSQLDIRY	rry 11			
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ID 07	042507	PRELIMINARY;	PRT;	8 AA.	

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Ognem5 toxoplasma Q9r735 streptomyce Q9ps68 gallus gall Q9k343 escherichia

Q9PS68 Q9K343

Q9N6M5 Q9R735

O9xmb4 aegilops ta

Q9xz42 albinaria h Q9u5j3 trypanosoma Q60517 mus musculu Q47251 escherichia Q78845 human immun

Q9TQY5 Q9URU0 Q66874 Q66877

Q47251 Q78845 Q9X242 Q9U5J3 Q60517

ACCOOCTOOLS ACCO

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SEQUENCE FROM N.A.
STRAIN=PIK.RED; TISSUE=PERICARP;
MEDLINE=91355936; PubMed=1715787;
Parsons B.L., Mattoo A.K.;
"Wound regulated accumulation of specific transcripts in tomato fruit:
interactions with fruit development, ethylene and light.";
Plant Mol. Biol. 17:453-464(1991).
EMBL; X59884; CAA42539.1;
                                                                                      Lycopersicon esculentum (Tomato).

Bukaryots, Viridiplantue; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rowen L., Qin S., Madan A., Loretz C., Hall J., James R., Dors M., Shaffer T., Abbasi N., Ratcliffe A., Dickhoff R., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility complex class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF110520; AAC9704.1; ·. .
NON TER 1.3 AS 1653 MW; 832A1D689E825B1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                 92CB257828733325 CRC64;
               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2000 (TrEMBLrel. 13, Last annotation update)
WOUND-INDUCED PROTEIN (FRAGMENT).
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Last annotation update)
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09TOY5;
01-MAY-2000 (TrEMBLrel. 13
01-MAY-2000 (TrEMBLrel. 13
01-MAY-2000 (TrEMBLrel. 13
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Best Local Similarity
Matches 3; Conserv
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6 DEYDY 10
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                                                                                                                                                                                                            STRAIN=CV MUSTANG;
MEDLINE=96189275; PubMed=8605312;
Joshl C.P., Kumar S., Nguyen H.T.;
Application of modified differential display technique for cloning and sequencing of the 3 region from three putative members of wheat HSP70 gene family.";
Plant Mol. Biol. 30:641-646(1996).
EMBL: L41507, ABB02333.1; -.
EMBL: L41505, ABB02333.1; -.
EMBL: L41066; ABB02332.1; -.
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                                                                                                    Triticum aestivum (Wheat).
Variaticum variationales, Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta, Liliopsida; Poales; Poaceae; Triticum.
NCBL_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96163501; PubMed=8566960;
Holder E., Maeda M., Bies R.D.;
"Expression and regulation of the dystrophin Purkinje promoter in
human skeletal muscle, heart, and brain.";
Hum. Genet. 97:232-239(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
DYSTROPHIN PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA; 886 MW; 71B2CB1B10532768 CRC64;
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                                                                HEAT SHOCK PROTEIN (FRAGMENT).
HSP70C OR HSP70A OR HSP70B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.8%;
75.0%;
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Best Local Similarity 37.5%;
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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4 VSSDEREM 11
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5 EEVD 8
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SEQUENCE
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STRAIN-255;
MEDLINE-95530311; PubMed-7732664;
Seal B.S., Neill J.D.;
"Capsid protein gene sequence of feline calicivirus isolates 255 and L.K.; further evidence for capsid protein configuration among feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Callciviridae;
Calicivirus.
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Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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Last annotation update)
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Pred. No. 8.5e+03;
1; Mismatches 5;
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MEDLINE-95250311; Pubmed-7732664;
                                                                                               caliciviruses.";
Virus Genes 9:183-187(1995).
EMBL; U07130; AAA74412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virus Genes 9:183-187(1995).
EMBL; U07131; AAA74415.1; -.
                                                                                                                                                                                                                  25.8%;
40.0%;
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Best Local Similarity 40.0
Matches 4; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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SEQUENCE
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GLYCOPROTEIN H-A N-TERMINAL, GPH-A N-TERMINAL=KEX2/SUBTILISIN-RELATED
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Calicivirus.
NCBI_TaxID=11978;
                                                                                                                          SEQUENCE.

MEDLINE-91340701; PubMed-1874725;
Christie D.L., Batchelor D.C., Palmer D.J.;
Christie D.E., Batchelor D.C., Palmer D.J.;
Identification of kex2-related proteases in chromaffin granules by partial amino acid sequence analysis.";
J. Biol. Chem. 266:15679-15683(1991).

SEQUENCE 12 AA; 1374 MW; 0BDF36703B5B1440 CRC64;
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Duesterhoeft A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PUTATIVE MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 3; Length 13;
Pred. No. 6.6e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AL022072; CAB64681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCD0A7CCD2FA36C6 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                 Score 18; DB 6; 1
Pred. No. 6.1e+03;
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066874
01-NOV-1996 (TEMBLEEL 01, L.
01-NOV-1996 (TEMBLEEL 01, L.
01-NOV-1998 (TEMBLEEL 08, L.
POLYMERASE (FRAGMENT).
Feline calicivius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%;
25.0%;
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66.7%;
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13 AA; 1456 MW;
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                                Bos taurus (Bovine).
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Best Local Similarity
Matches 4; Conserv
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Matches 2; Conserv
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SEQUENCE FROM N.A.
MEDLINE-87213162; PubMed=3579900;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Clausiliidae; Alopiinae; Albinaria.
NCBI_TaxID=69418;
                                                                                                                                                   Gaps
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         Jordan P.M., Mgbeje B.I.A., Alwan A.F., Thomas S.D.; Mulleotide sequence of hemD, the second gene in the hem operon of Escherichia coli K.12... Nucleic Acids Res. 15:10583-10583(1987).
                                                                                                                                                                                                                                                                                                                                                                                           Wong-Staal F., Gallo R.C., Chang N.T., Ghrayeb J., Papas T.S., Lautenbegger J.A., Pearson M.L., Petteway S.R. Jr., Ivanoff L., Bammeister K., Whitehorn E.A., Rafalski J.A., Doran E.R., Josephs S.J., Starcich B., Livak K.J., Patarca R., Haseltine W.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12;
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                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Van Beveren C.P., Coffin J., Hughes S.;
(In) Weiss R.L., Teich N., Varmus H., Coffin J. (eds.);
RNA tumor viruses, second edition, 2, pp.2:1102-1123,
Cold Spring Harbor Laboratory Press, New York (1985).
                                                                                          5D2DE8339BA045B3 CRC64;
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12 AA; 1266 MW; 8FE6D0408CBAA865 CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
REV PROTEIN (FRAGMENT)
HUMAN immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Last annotation update)
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MEDLINE=88096587; PubMed=3320969;
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                                                        EMBL; Y00883; CAA68775.1; -. NON_TER 1 1
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NON_TER 12
SEQUENCE 12 AA; 1266 MW;
                                                                                        SEQUENCE 12 AA; 1375 MW;
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75.0%;
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01-NOV-1999 (TrEMBLrel, 12,
01-NOV-1999 (TrEMBLrel, 12,
01-OCT-2000 (TrEMBLrel, 15,
                                                                                                                                                   4; Conservative
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                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
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[1]
SEQUENCE FROM N.A.
Schilthuizen M., Hoekstra R.F., Gittenberger E.;
Schilthuizen maintenance of a rare CaM haplotype in a land snail hybrid
"Selective maintenance of a rare CaM."
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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NCBL_TaxID=5691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Webb H.D., Gaud A.F., Carrington M.; "The trypanosoma brucei GPI-PLC gene is not linked to functionally related genes or to genes showing the same developmentally regulated expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 1e+04;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                           Length 13;
                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF132317; AAD34387.1; -.
HSSP; P02593; IAJI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250727; CAB60092.1; -.
Heat shock.
                                                                                                                                                                                                                                                             13 AA; 1463 MW; A7BDD19BBA114056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AA; 1524 MW; 37C19EC3787FA728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HEAT SHOCK PROTEIN 100 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
(FRAGMENT).
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Pred. No. 1e+04;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AA.
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Eukaryota: Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
Toxoplasma.
NCBI_TaxID=5811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-RH, COUGAR TC751G34, SEA OTTER TC828G1, AND BEVERLEY;
Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;
"Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and Housekeeping Genes.",
J. Parasitol. 0:0-0(2000).
BMBL; AF249695; AAF79153.1; -.
EMBL; AF249693; AAF79153.1; -.
EMBL; AF249693; AAF79150.1; -.
EMBL; AF249694; AAF79151.1; -.
EMBL; BF249694; AAF79152.1; -.
EMBL; BF249695; AAF79150.1; -.
EMBL; BF24
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
Koiwai O., Kaneda T., Morishita R.; Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in mammalian cells."; Biochem. Biophys. Res. Commun. 144:185-190(1987). Transferase. 1 Transferase. 1 13 13 SEQUENCE 13 AA; 1508 MW; 53F7C770F617BAA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                Score 17; DB 11; Length 13;
Pred. No. 1e+04;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.2%; Score 16; DB 5; Length 8; Best Local Similarity 75.0%; Pred. No. 3.7e+05; Matches 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DIHYDROFOLATE REDUCTASE THYMIDYLATE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                             Query Match 25.8%;
Best Local Similarity 60.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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3 QTELD 7
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Q9N6M5;
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Q9N6M5
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Search completed: January 17, 2001, 13:36:13 Job time: 108 sec

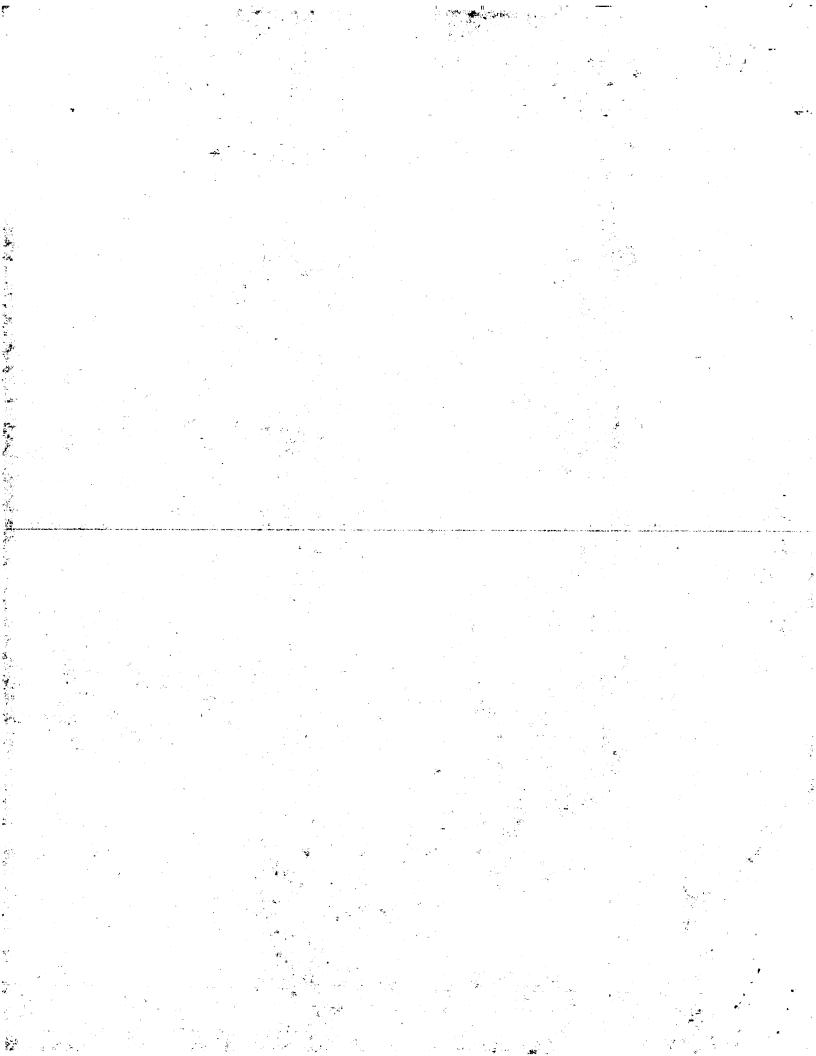
9 EEID 12 :||| 3 KEID 6

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Gaps

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COMPUTER READABLE FORM:
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Sequence 22, Appl
atent No. 5395759
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Sequence 9, A
Sequence 3, A
Sequence 4, A
Sequence 17,
Sequence 11, A
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Sequence 3
Sequence 3
Sequence 3
Sequence 1
Sequence 1
Sequence 1
Sequence 6
Sequence 6
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Sequence 8
Sequence 8
Sequence 9
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Sequence 9
Sequence 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
.: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  Compugen Ltd
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US-08-441-935-22

US-08-140-137A-17

US-08-119-361-3

US-08-518-967-7

US-08-518-967-7

US-08-518-967-7

US-08-318-856A-3

US-08-318-856A-3

US-08-318-856A-3

US-08-318-856A-3

US-08-318-856A-2

US-08-318-856A-
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US-08-318-970B-8
US-08-140-137A-3
US-08-603-753D-9
US-08-603-753D-10
                                                                                                                                                                                                                                                                                                                                              Potal number of hits satisfying chosen parameters:
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                          174772 seqs, 17957048 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           January 17, 2001, 13:26:41
                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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66
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0 Maximum DB seq length: 13
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Perfect score:
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                                                                         OM protein -
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                                                                                                                                                                                                                       Sequence:
                                                                                                           Run on:
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No.
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29 22 33.3 10 3 US-09-099-753-9 Sequence 9, Appl. 3 US-09-099-753-10 Sequence 10, Appl. 3 US-09-099-753-10 Sequence 10, Appl. 3 US-09-099-753-10 Sequence 50, Appl. 3 US-09-09-753-5555 Sequence 50, Appl. 3 US-08-704-170-18 Sequence 18, Appl. 3 US-08-040-216-39 Sequence 18, Appl. 3 US-09-040-216-39 Sequence 18, Appl. 3 US-09-040-216-39 Sequence 19, Appl. 3 US-08-10075-13 Sequence 19, Appl. 3 US-08-10075-13 Sequence 3, Appl. 4 US-08-162-081B-3 Sequence 6, Appl. 4 US-08-162-081B-3 Sequence 6, Appl. 4 US-08-162-081B-3 Sequence 6, Appl. 4 US-08-162-081B-3 Sequence 8, Appl. 4 US-08-122-8 Sequence 18, Appl. 4 US-08-122-8 Sequence 18, Appl. 4 US-08-325-071-18 Sequence 18, Appl. 4 US-08-325-071-18 Sequence 25, Appl. 4 US-08-742-243-25 Sequence 25, Appl. 4 US-08-742-243-25 Sequence 25, Appl. 4 US-08-742-243-25
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ALIGNMENTS

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US-00-14.1-935-28

US-00-14.1-935-28

Sequence 28, Application US/08441935

Patent No. 660447

GENERAL INFORMATION:

APPLICANT: CHAPMAN BARBARA

APPLICANT: BURKE, RAE LIN

APPLICANT: MIKELSON, JAN MOLLER

TITLE OF INVENTION: ACTIVITY AND PRODUCTION THERDOF

TITLE OF INVENTION: ACTIVITY AND PRODUCTION THEREOF

CORRESPONDENCE ADDRESS: 31

CORRESPONDENCE ADDRESS: 31

CORRESPONDENCE ADDRESS: 31

CORRESPONDENCE ADDRESS: 31

CORPESSE: REED 6 ROBINS

STREET: 285 HAMIITON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTY: UNITED STATES OF AMERICA

COUNTY: UNITED STATES OF AMERICA

COMPUTER: IN PC COMPALIA

COMPUTER: IN PC COMPALIA

COMPUTER: IN PC COMPALIA

COMPUTER: IN PC COMPALIA

MEDIUM TYPE: FLORDY disk

COMPUTER: IN PC COMPALIA

APPLICATION NUMBER: US 08/266,170

FILING DATE: 16-MAY-1995

CLASSIFICATION NUMBER: US 07/652,099

FILING DATE: 7-FEB-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/652,989

FILING DATE: 17-MAY-1987

APPLICATION NUMBER: US 07/652,989

FILING DATE: 17-MAY-1987

APPLICATION NUMBER: US 06/822,989

FILING DATE: 17-MAY-1987

REFERENCE/DOCKET NUMBER: 33,208

REFERENCE
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0;

5

Pred. No. 11; 0; Mismatches

75.0%;

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6; Conservative
   Best Local Similarity
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                                                                                                                                                        4 RTXLQXDQ 11
                                                                                                             1 RTTLQSDQ 8
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US-08-140-137A-17
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                                       Matches
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UG-08-441-935-22
Sequence 22, Application US/08441935
Sequence 22, Application US/08441935
Patent No. 6060447
GENERAL INFORMATION:
APPLICANT: BURKE, RAE LYN
APPLICANT: RASMUSSEN, MIRELIA EZBAN
APPLICANT: RASMUSSEN, MIRELIA EZBAN
APPLICANT: MIKKELSON, JAN MOLLER
TITLE OF INVENTION: PROTEIN COMPLEXES HAVING FACTOR VIII:C
TITLE OF INVENTION: ACTIVITY AND PRODUCTION THEREOF
                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELLING DATE: US/08/441,935
FILING DATE: 16-MAY-1995
                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 311111 AND FRODOLOGY
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STRATE: CALIFORNIA
COUNTY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPUTE
                                                                                                                                                                                                                       Score 34; DB
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROBINS, ROBERTA
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 2300-0048.11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/652,099
FILING DATE: 7-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/051,916
FILING DATE: 19-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/822,989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 22.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       51.5%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-JAN-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       Query Match 51.5
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 amino acids
                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-441-935-28
   single
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STRANDEDNESS: sir
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STRANDEDNESS:
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DB 3; Length 11;

45.5%; Score 30;

Query Match

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## PATENT NO. 5395759

*PATENT NO. 5395759

*PATENT NO. 5395759

*PATENT NO. TOWNER, IAN H.; DYALL-SMITH, MICHAEL L.

**AITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCE

**ENCOLING THE HUMAN ROTAVINGS MAJOR OUTER CAPSID GLYCOPROTEIN

NUMBER OF SEQUENCES: 14

**CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 5; Length 12;
Pred. No. 93;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: TUORANEN, ELAINE
APPLICANT: TUORANEN, H. R.
TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE
TITLE OF INVENTION: ADHESION MOLECULE (ELAM)
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,137A
FILING DATE: 27-MAY-1994
CLASSIFICATION: 424
ATTORNEY/ACTIVE
                                                                                                                                                                 APPLICATION NUMBER: US/07/474,642
FILING DATE: 29-APR-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 824,704
FILING DATE: 04-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 17, Application US/08140137A ; Patent No. 5817617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 13 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.9
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Sequence 9, Application US/08197793
Sequence 9, Application US/08197793
Sequence 9, Application US/08197793
Sequence 9, Application US/08197793
Sequence 9, Application Sequence Schraven, B.
APPLICANT: Schraven, B.
APPLICANT: Schoenhaut, D.
APPLICANT: Ratnofsky, S.
TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                 Sequence 7, Application US/08518967
Patent No. 5861307
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN S-WC-LIKE POLYPEPTIDE AND
TITLE OF INVENTION: A GENE CODING FOR SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORDERSPENDENCE ADDRESS:
ADDRESSEE: NIELDS & LEMACK
STREET: 176 East Main Street, Suite 8
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,967
FILING DATE: August 24, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-207236
FILING DATE: 31-AUG-94
ATTORIEY/AGENT IRFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.4%; Score 24; DB 2; I ilarity 71.4%; Pred. No. 1.1e+02; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lemack, Kevin S.
REGISTRATION NUMBER: 32,579
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 898-1818
TELEFAX: (508) 898-2020
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-518-967-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 60 STATE STRI
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                          STREET: 176 East
CITY: Westboro
STATE: Massachu:
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 SDQEEID 12
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3 SEGEEID 9
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08119361
Patent No. 5523390
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan
APPLICANT: Parloff, Nadine
TITLE OF INVENTION: Porphyromonas gingivalis Arginine-specific Proteinase
NUMBRE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
                                                                                                                                                                                             ö
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels
                                                                                                                                               Length 13;
                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,361
FILING DATE: 10-5EP-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FGLDEY DOOM M.
REGISTRATION NUMBER: 31878
REFERENCE/DOCKET NUMBER: 21-93
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 303-499-8089
                                                                                                                                               Score 25; DB 2;
Pred. No. 1e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.4%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                             Query Match 37.9%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.4
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FRAGMENT TYPE: internal US-08-119-361-3
                                                               internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                   2 TTLQSDQEEIDY 13
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| TLVAIQNEEIEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TLQSDQEEI 11
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                                                             ; FRAGMENT TYPE:
US-08-140-137A-17
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US-08-119-361-3
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Gaps
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                                                                                                                                                                                                                                                              Length 11;
                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                            Score 24; DB 2;
Pred. No. 1.3e+02;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/197,793
ATTORNEY/AGENT INFORMATION:
NAME: DECORTÍ, GIULIO A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-006CPPC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOUR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
TITLE OF INVENTION: pp32: A Newly Ide
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application PC/TUS9501618 GENERAL INFORMATION:
  TELECOMMUNICATION INFORMATION
                  TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                              36.4%;
42.9%;
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 42.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
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                                                                                                                                                           MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-636-176-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Matches 3; Conserva
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MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                         7 DQEEIDY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 DQEEIDY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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PCT-US95-01618-9
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APPLICANT: Schraven, B.
APPLICANT: Schoenhaut, D.
APPLICANT: Retnofsky, S.
TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 1; Length 11; Pred. No. 1.3e+02; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,019; 08/004,199
FILING DATE: 19-APR-1991; 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, GUILLO A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-006CNCP
                                                                                  PILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,019;
FILING DATE: 19-APR-1991
APPLICATION NUMBER: 08/004,199
FILING DATE: 13-AN-1993
ATTORNEY AGENT INFORMATION:
NAME: DECONTI, Giulio A., Jr.
RECISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-006CNCP
TELECOMNUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-7541
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/636,176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: LAHIVE & COCKFIELD
60 STATE STREET, SUITE 510
                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,793
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08636176
Patent No. 5846822
GENERAL INFORMATION:
APPLICANT: Meuer, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 42.9%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-197-793-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2(CORRESPONDENCE ADDRESS:
                                       ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DQEEIDY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1::: | |
2 DEQDIDY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
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STREET: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Ouery Match 34.8
Best Local Similarity 50.0
Matches 3; Conservative
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ORIGINAL SOURCE:
ORGANISM: Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-FEB PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                  STATE: D.C. COUNTRY: U.S.A. ZIP: 20006
           STREET: 2033 K SI
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: Sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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3 KDELDY 8
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PCT-US95-02121-17
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US-08-318-856A-3

US-08-318-856A-3

Sequence 3, Application US/08318856A

Patent No. 5972351

GENERAL INFORMATION:

APPLICANT: Adrian V.S. Hill, et al.

TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-

TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE

TITLE OF INVENTION: ANTIGENS (AS AMENDED)

NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08318856A
Patent No. 5972331
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1993
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATORNEY/AGENT INFORMATION:
NAME: Lee Chang
REFERENCE/DOCKET NUMBER: 263-PPIR1577US
TELEPHONE: (202) 721-8200
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
TELEFAX: Amin, acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 2;
Pred. No. 1.3e+05;
                                                                                                                                                                                                                     ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Plasmodium falciparum
US-08-318-856A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.8%;
50.0%;
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Best Local Similarity 50.0
Matches 3; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                 U.S.A.
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3 KDELDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 2; Length 8;
Pred. No. 1.3e+05;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APril 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REGISTRATION NUMBER: 263-PPIRI577US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1009
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH 8 mainto acid residues
E: Wenderoth, Lind & Ponack, L. 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/318,856A FILING DATE: October 3, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: PCT/US95/02121
16-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS ANI TITLE OF INVENTION: CTL IMMUNITY NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC CCMPATIBLE OPERATING SYSTEM: PC-DOS/MEDS SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application PC/TUS9502121
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STRTE: 12202
LIP: 22202
COMPUTER: VITALIAN STREET: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: WS/08/080,240
FILING DATE: 19930622
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5312750ma F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.8%; Score 23; DB 1; Length 9; 50.0%; Pred. No. 1.3e+05; 1ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                      Score 23; DB 1; I
Pred. No. 1.3e+05;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08080240; Patent No. 5312750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703)413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ONO, HIROKI
APPLICANT: ISHTANI, YOSUKE
APPLICANT: TSUMORA, MANA
APPLICANT: IWAMI, MORITA
APPLICANT: KOJO, HITOSHI
                                                                                                                                                                                                                                                        34.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ARAMORI, ICHIRO
APPLICANT: FUKAGAWA, MASAO
                                                                                                                                           ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-07-779-049-1
    TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 50...
4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                   LENGTH: 9 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703)413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.8
Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMINO ACID
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-08-080-240-1
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22222
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 4; Length 8; Pred. No. 1.3e+05; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/779,049
FILING DATE: 199911018
                                                                                                               APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/POCKET NUMBER: 14137-26-4PC
TELEPHONE: (206) 467-9600
TELEPHONE: (215) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 07/935,811 FILING DATE: 26-M02-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/874,491 FILING DATE: 27-APR-1992
PRIOR APPLICATION NUMBER: US 07/827,682 APPLICATION NUMBER: US 07/827,682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 18-723-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Oblon, No. 5310659man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/07779049
Patent No. 5310659
GENERAL INFORMATION:
APPLICANT: ARAMORI, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUKAGAWA, MASAO
ONO, HIROKI
ISHITANI, YOSUKE
TSUMURA, MANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IWAMI, MORITA APPLICANT: KOJO, HITOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-17
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 QEEIDY 13
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RESULT 15
US-08-318-856A-20
Sequence 20, Application US/08318856A
Sequence 20, Application US/08318856A
Sequence 20, Application US/08318856A
Tarent No. 597231
GEMERAL INFORMATION
TILE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS ITILE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS ITILE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
ZIP: 20006
ZIP: PARDABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
SOFTWARE: Wordberfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: April 3, 1992
PRIOR APPLICATION NUMBER: 20, 1992
PRIOR APPLICATION NUMBER: 40, 999
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40, 949
REFERENCE/DOCKET NUMBER: 203-PPIR1577US
TELEPHONE: (202) 721-8200
TELEPHONE: (202) 721-8250
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERESTICS:
LENGTH: 9 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STARNDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-856A-20
QSDQEEID 12
                       8 QEEIDY 13
                                        Д
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Search completed: January 17, 2001, 13:34:39 Job time: 478 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:34:45 ; Search time 25.93 Seconds (without alignments) 21.099 Million cell updates/sec Run on:

US-08-765-837-2 84 Perfect score: Sequence:

1 DEDENQSPRSFQKKTR 16

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

268485 seqs, 34193795 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

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/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp/AA1987.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:* /SIDS1/gcgdata/geneseg/genesegp/AA1994.DAT:*/SIDS1/gcgdata/geneseg/genesegp/AA1995.DAT:*/SIDS1/gcgdata/geneseg/genesegp/AA1996.DAT:* /SIDSI/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDSI/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDSI/gcgdata/geneseq/geneseqp/AA2000.DAT:* A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score		Query Match Length DB ID	DB	ID	Description
-	84	100.0	16		R90946	Factor VIII antige
7	31	36.9	11	6	P81967	Peptide immunogen
٣	30	35.7	σ	17	R94901	Tastin antiqen. H
4	30	35.7	13	19	W33005	Murine DP-3 protei
S	30	35.7			W29907	Porcine AMPK-alpha
9	29	34.5			R84179	MKK1 C-terminal pe
7	28	33.3			W37161	Human TcAK1 antibo
80	28	33.3	14	18	18 W14614	Human antithrombin
6	27	32.1	6	17	W49604	Human leucocyte an
10	27	32.1			W87479	HIV-1 mutant env q
11	27	32.1	•		P70148	N-terminal of S3-q
12	26	31.0	13		R60988	CD4 cvtoplasmic do

	Human DC12 proto-o	Natural 17 Occur 21		STAT3 inhibition c	Antigenic oligopep	Apolipoprotein B-1	STAT3 inhibitory p	N-Terminal sequenc	Non-immunogenic am	Apolipoprotein B-1	Neutrophil -activat	Human cytohesin-1	Leptin receptor C-	Protein kinase C-d	GAL4 activation do	Immunogenic peptid	GAL4 activation do	Sona pellucida pro	Chemokine tumour a	Rainbow trout Ladd	EBV tegument prote	HIV-1 MO/LAI env g	Peptide from EBV t	Epitopmprising	Human sciellin pep	HLA class II bindi	HLA class II bindi	Rainbow trout ladd	2	4	Mitochondrial loca	la t	Cadherin-7 cell ad
-	Y 21230	n .	R70619	R73639	P70536	R46995	R73630	R69370	P90817	R47035	Y50238	W54304	W37419	W17479	Y52115	Y46140	Y52103	W36122	Y29892	Y68402	R49476	W87485	W54680	W35276	Y32031	Y98859	Y98956	Y68387	R66025	R66026	\circ	50	Y61439
	א כ			16	æ	15	1.6	16	10	15	20	19	18	18	20	20	20	19	20	21	15	19	19	18	20	21	21	21	15	15	16	19	21
	٦ - د ت	7	Q,	12	13	13	13	14	15	15	15	7	89	o,	σ	6	10	11	11	11	13	13	13	15	15	15	15	15	16	16	16	16	ហ
	9 0			٠.	8		8.6			8.6	8.6			9.6			9.6	9.6	9.0			٠,	9.6		9.6	9.6	9.0	9.6		9.6	9.0	9.8	7.4
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	7 -	# I	7	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT R90946

R90946 standard; peptide; 16 AA

R90946;

09-SEP-1996 (first entry)

Factor VIII antigenic peptide corresp. to residues Asp1681-Arg1696

Factor VIII; modification; inhibitor activity; binding; antibody; von Willebrand factor; immune disorder.

Synthetic.

WO9602572-A2 01-FEB-1996.

16820-

R

95WO-BE00068 14-JUL-1995;

94BE-0000666. 14-JUL-1994;

(CROI-) CROIX ROUGE BELGIQUE.

Laub R; Di Giambattista M,

WPI; 1996-105861/11.

Factor VIII antigenic polypeptide fragments and epitope(s) - also inhibitors of factor VIII and anti-inhibitors, useful for e.g. preventing and treating immune disorders involving inhibition of factor VIII binding

Claim 8; Page 31; 45pp; French.

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R94901 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.7%;
62.5%;
                                                                                                                                                                                                                    95US-0439818.
                                                                                                                                                                                                  95WO-US13259
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.50,
Local 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                       WPI; 1996-209192/21
                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
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1 dqenqdpr 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EDENQSPR 9
                                                                              Tastin antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9743647-A1.
                                                          03-JUL-1996
                                                                                                                                         Homo sapiens
                                                                                                                                                          WO9610414-A1
                                                                                                                                                                                                  04-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1998
                                                                                                                                                                                                                     12-MAY-1995;
                                                                                                                                                                                                                               04-OCT-1994;
                                                                                                                                                                              11-APR-1996
                                                                                                                                                                                                                                                                     Fukuda MN;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                       R94901;
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 RESULT
R94901
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        Peptides R90945-64 are derived from the factor VIII protein, esp. from a modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to on Willebrand factor, esp. antibodies, thus preventing or treating immune disorders.
                                                                                                                                                                                                                                                                                                Human papilloma virus; immunogen; antibody; antigen; cervical carcinoma; HPV-16; early reading frame; E4.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic peptide(s) of human papilloma virus - corresp. to amino acid sequence region having at least one reverse turn and predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The peptide corresponds to amino acids 48-58 of the E4 early open reading frame of HPV-16. It can be used to raise antibodies for vaccines or to heighten the immune response to an HPV infection
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0
                                                                                                         Length 16;
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                                                                                                                              Indels
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                                                                                                         100.0%; Score 84; DB 17;
100.0%; Pred. No. 4.2e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             (STRD ) LELAND STANFORD JUNIOR UNIVERSITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 13; 27pp; English.
                                                                                                                                                                                                                  P81967 standard; protein; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.98;
40.08;
                                                                                                                                                                                                                                                                                                                                                                                       87EP-0306061
                                                                                                                                                                                                                                                                                                                                                                                                         87US-0884184
                                                                                                                                                                                                                                                         16-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                             Peptide immunogen for HPV
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                                                                                                                              Conservative
                                                                                                                                                           1 DEDENOSPRSFOKKTR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1988-057971/09.
                                                                                                          Query Match
Best Local Similarity
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|::|:|
1 dqdqsqtpet 10
                                                                             16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hydrophilicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                already present
                                                                                                                                                                                                                                                                                                                                                                                                                                                Schoolnik GK,
                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-1987;
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                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                               EP257754-A.
                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                             Sequence
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                                                                                                                                                                                                                                       P81967;
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                                                                                                                              Matches
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Gaps
Trophinin; trophinin-assisting protein; tastin; bystin; lastin; embryo implantation; infertility; cell adhesion; therapy; diagnosis; antibody.
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s of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A peptide (R94901) corresponding to amino acids 41-49 of huma trophinin-assisting protein tastin (see also R94900), and representing an active fragment of tastin, was used to discentibodies in rabbits. These antibodies were used to united
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 17; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assaying; cell cycle regulator; E region; DP-3 protein; nuclear localisation signal; 'NLS; mouse; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammallan trophinin and trophinin-assisting protein - u inhibiting or enhancing embryo implantation, diagnosis infertility and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tastin in samples of cells and tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine DP-3 protein derived peptide.
                                                                                                                                                                                                                                                                                                                                (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; Page 80; 106pp; English.
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This sequence represent a biologically active peptide derived from the 5'-AMP-activated protein kinase (AMPK) catalytic alphal subunit from pig liver. This fragment retains at least one of the activities of native. AMPK-alphal i.e the ability to stimulate phosphorylation of picinin molecules and the ability to mimic the binding of native AMPK-alphal i.e the ability to mimic the binding of native AMPK-alphal to at least one antibody or ligand molecule. AMPK polypeptides can be used to identify compounds which regulate the action of kinases. Such fragments can be used to reduce biosynthesis of cholesterol and intity acids. They may also be used to inhibit the release of these molecules from intracellular stores by hormone sensitive lipses (HSL). They may also be used to reduce cellular malonyl CoA levels and promote the beta-oxidation of fatty acids by mitochondria. AMPK-alphal fragments could be used in the treatment of e.g. hypercholesterolaemia, coesity, clinical syndromes associated with hypoxia or ischaemia (e.g. myocardial infarction) disorders of nutrition and
                               develop products for treating e.g. hyper-cholesterolaemia, obesity, hypoxia, ischaemia, nutrition disorders or diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New poly:nucleotide(s) encoding megakaryocyte tyrosine kinase(s) used to develop prods. for the treatment and diagnosis of kinase related signal transduction abnormalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18; Length 16; 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase; cellular signal transduction; leukaemia; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                             New isolated 5'-AMP-activated protein kinase subunit(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30;
Pred. No. (
                                                                                             Disclosure; Page 36; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Page 41; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ullrich A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R84179 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-382959/49.
 WPI; 1997-372811/34.
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| dekesrrlfqq 11
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               16 AA;
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R84179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                   Assays for identifying regulators of cell cycle progression -
comprise expressing a protein having a transcription factor nuclear
localisation signal and determining the degree of nuclear
                                                                                                                                                                                                                                                                            The present sequence was used in the development of a novel assay comprises expressing in a cell a protein comprising the E region and sufficient C-terminal residues of a DP-3 protein to provide a functional nuclear localisation signal (NLS), or the NLS of E2F-1, and a marker for nuclear localisation. Then the degree of nuclear localisation in the presence and absence of the putative regulator is determined. Regulators identified using the assay can be used as potential regulators of cell proliferation, or as models for rational drug design. Regulation of the NLS may lead to effects such as enhanced cell division, blocking of cell cycle progression or apoptosis. The regulators may also be used to design other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Witters LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porcine AMPK-alphal active peptide fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 1
Pred. No. 49;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kemp BE, Mitchelhill KI, Stapleton DI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [DART-] DARTMOUTH COLLEGE.
|SVIN-] ST VINCENTS INST MEDICAL RES.
                                                                                                                                                                                                                                                    Example 1; Page 17; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W29907 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          candidate regulatory compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.7%;
50.0%;
                                                                                                          De La Luna S, La Thangue NB;
                                             96GB-0010195;
              97WO-GB01324.
                                                                           (MEDI-) MEDICAL RES COUNCIL.
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                                                                                                                                      WPI; 1998-009053/01.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AA;
              15-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-1996;
                                            15-MAY-1996;
                                                                                                                                                                                                                    localisation
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Gaps

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                                                                                                                         5; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-231188/21.
                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                   1 DEDENQSPRS 10
                                                                                                                                                                    ||:: |||
4 denkeakprs 13
                                                     13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 deden
                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases
                                                                                                                                                                                                                                                                           W14614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease
                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
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                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                    W14614
 SSSX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human twenty-five C associated protein kinase I (TcAKI) antibody internal C-terminal peptide from the present invention. The present invention also describes: creating a creating an expect invention. Bubstrate by incubating the substrate in a cell transformed with the TaCKI DNA sequence, such that a 14-3-3 recognition motif is created in the substrate in a 14-3-3 protein on a 14-3-3 protein or a TcAKI substrate, where the mutation prevents or interferes with phosphorylation-specific interaction between the 14-3-3 protein and the TcAKI substrate, by: (a) incubating the 14-3-3 protein and the TcAKI substrate which is suspected of being mutated in a cell transformed with the TcAKI DNA sequence such that the 14-3-3 protein and the TcAKI substrate which is suspected of being mutated in a cell transformed with the TcAKI DNA sequence such that the 14-3-3 protein and TcAKI substrate of interaction with the level obtained with a non-mutant component, and (c) diagnosing a mutation in either the 14-3-3 protein or TcAKI substrate with the nevel of interaction differs significantly from the level obtained with the non-mutant components. TcAKI has a role in mediating interaction between 14-3-3 proteins involved creates a 14-3-3 recognition motif and other cellular proteins involved
                                                                                                                                                                 .;
0
           Synthetic peptides (R84179-80) corresponding to the C-terminal regions of novel human megakaryocytic kinases MKK1 (R84181) and MKK2 (R84182) were used to raise anti-MKK antibodies capable of immunoprecipitation of in vitro transcribed and translated MKK1 and
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding Twenty-five C Associated protein Kinase 1 - useful for, e.g. detecting cancers or disorders of cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                 Human; twenty-five C associated protein kinase 1; TcAK1; detection;
cancer; cell proliferation; Cdc25; phosphorylation; 14-3-3 protein;
                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                      Human TcAK1 antibody internal C-terminal peptide SEQ ID NO:16.
                                                                                                                               DB 16; Length 15;
                                                                                                                                                              3; Indels
                                                                                                                                   Score 29; DB 1
Pred. No. 85;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 48; 75pp; English.
                                                                                                                                                                                                                                                                                    W37161 standard; peptide; 13 AA.
                                                                                                                                   34.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US11721
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                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
                                                                                                                    Query Match
Best Local Similarity
The 6; Conserve
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                                                                                                                                                                                         1 DEDENQSPRS 10
                                                                                                                                                                                                         | | : ||||
3 dadgstsprs 12
                                                                                            15 AA;
                                                                    MKK2 proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9801756-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                               cancer; ce
antibody.
                                                                                             Sequence
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in oncogenesis and signalling events. Measurement of protein binding at TCAK1-mediated 14-3-3 recognition sites can be used to direct cancers or other disorders of cell proliferation.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human antithrombin III mutant with C-terminal peptide containing a sulphated tyrosine - useful for treatment and prevention of thrombic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human antithrombin III (AT III) mutant, comprising a carboxy-terminal sulphated tyrosine peptide extension, i.e. the present peptide, can be used to prevent and/or treat thrombotic
                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; antithrombin III; mutant; carboxy-terminal; extension; sulphated tyrosine; prevention; treatment; thrombosis; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "carboxy-terminus of wild type human antithrombin III"
                                                                                                                                                                                                    Score 28; DB 19; Length 13;
Pred. No. 1.1e+02;
Wismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human antithrombin III carboxy-terminal extension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2e+02;
hes 0;
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100.0%; Pred. No. 1.2e+02
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W14614 standard; peptide; 14 AA.
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W49604
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us-08-765-837-2.closed.rag

W49604;

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The mutations result in non-infectious HIV-1 particles. Inactive, protease-deficient HIV-1 particles containing at least one of Nef truncated protein fragments are used as immunogens, particularly for reducing or preventing apoptosis in HIV-1 sero-negative or positive subjects, specifically those with HIV-1 infection, both for preventing and treatment. Fragments of nef gene and fragments encoding specific mutant Nef proteins are also useful in hybridisation tests for diagnostic detection of mutated genes in (lysed) cells or body fluids, while the antibodies. The proteats are detected in immunoassays using antibodias. The protease deficient HIV-1 particles and antibodies, optionally attached to a radiolosotope, chemotherapeutic agent or toxin, can be used to reduce the severity of HIV infections.
                                                                                                                                                                                                                                                                           the defective human immunodeficiency virus-1 (HTV-1) provirus in L-2 cells. They represent the portions of pol protease (prot.), vpr. env (9p120 and 9p41), and nef gene regions that were mutated as compared type HTV-1 in LAI or MOVIAI cells. The invention relates to mutuched DNA, proteins or fragments of defective HIV-1 provirus in L-2 cell line.
                                                                                                             New nucleic acid encoding mutant or truncal {}^{i,j} torms of human immune deficiency virus proteins - used to generate non-infectious particles useful as therapeutic or prophylactic immunogens, also for
                                                                                                                                                                                                                                                               Sequences W87475 to W87463 represent mutant amino acid sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Self incompatibility; S-protein; pollen tube; style; stigma; pollination; gametocide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crawford RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.1%; Score 27; DB 19; Length 13;
Clarity 41.7%; Pred. No. 1.6e+02;
Closervative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson M, Cornish E, Tregear GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal of S3-genotype-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P70148 standard; peptide; 15 AA.
                                                                                                                                                                                                                       Example 1; Fig 1; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85US-0854139.
85US-0792435.
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2 eesqnqqerneq 13
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                                                            WPI; 1998-568304/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AA;
                                                                                   N-PSDB; V71862
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                        Luftig RB;
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Niall HD;
                                                                                                                                                                                    diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This peptide is an example of a peptide which binds to a human leucocyte antigen HLA-D04 molecule. The peptide was isolated from a phagemid combinatorial library comprising the sequence V05953, by screening with an HLA-D04 molecule. The peptide is used for the treatment of autoimmune disease, or especially for treatment of viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus-1; HIV-1; protease; provirus; L-2 cell;
mutation; Nef protein; immunogen; apoptosis; treatment; hybridisation;
cell lysis; chemotherapeutic; toxin; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-binding oligopeptide and an immuno:regulator contg it - used in the treatment of auto:immune disease
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                                                                                                                                                       Human leucocyte antigen; HLA-DQ4; combinatorial library; autoimmune disease; chronic articular rheumatism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1 mutant env gp41 amino acid fragment in L-2 cell.
                                                                                                                    Human leucocyte antigen DQ4 binding peptide #495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 53; 61pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W87479 standard; peptide; 13 AA.
W49604 standard; peptide; 9 AA
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62.5%;
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Best Local Similarity 62.30,
Hara 5; Conservative
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                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                        (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
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                                                                            05-JUN-1998
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                                                                                                                                                                                                                                                                                                                                       28-NOV-1994;
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                                                                                                                                                                                                                     Synthetic.
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WB7479;

RESULT 10 W87479

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Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; bown's syndrome; myothonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament L; neurofilament meurofilament E; presenilin II; presenilin II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift
The interaction of a lipid kinase, such as PI 3-kinase or PI 4-kinase, with CD4-P56lck, may be blocked by administering a peptide. This peptide may be a fragment of the cytoplasmic domain of CD4 (eg R60987-R60991), a fragment of p56lck (eg R60992, R60993), a fragment of PI 3-kinase (eg R60994, R60995), or a fragment of PI 4-kinase. Other proline-rich peptides that bind to SH3 binding sequences can also be used, such as the fragment of 3BPI protein that binds to the SH3 of the AbI kinase (R60997), or a sequence found in the SOS protein (R60999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     high mobility group protein-C; neuroendocrine specific protein A
                                                                                                                                                                                                                                                                 Score 26, DB 15, Length 13;
Pred. No. 2.4e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                           2.4e+02;
...c 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bcl2 proto-oncogene mutant protein fragment 78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYUT-) RIJKSUNIV UTRECHT.
(ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y21230 standard; Protein; 13 AA.
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                                                                                                                                                                                                                                                                 31.0%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0043163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-IB00705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                 Query Match 31.0
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-609901/51.
                                                                                                                                                                                                          13 AA;
                                                                                                                                                                                                                                                                                                                                            6 QSPRSFQK 13
                                                                                                                                                                                                                                                                                                                                                                                 5 gcphrfgk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; X75766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9845322-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burbach JPH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-0CT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y21230;
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y21230
        888888888888%8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In order for certain T cells to make an optimal response to antigen, it is necessary for the T cell surface antigen CD4 to couple to the protein-tyrosine kinase p551ck. (CD4-p561ck is known to associate with and functionally synergise with the TCR/CD3 complex.)CD4-p561ck complex in T cells associates with two lipid kinases significant and P1 4-kinase, which suggests that these lipid kinases are also involved in intracellular signalling via the T cell receptor complex.
                                                                                                                                                           The sequence was used as a basis for the design of probes to isolate DNA encoding the S proteins. The sequence was determined by conventional microsequencing techniques performed on protein purified from styles dissected from the flowers of the plant. The S-proteins control the self-incompatibilty reaction. They are useful in control of pollen tube growth egas natural gametocides to control, induce or promote self-incompatibilty and interspecific incompatibilty. See also P70149-P70154, N70219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for inhibiting or reducing signal transduction – utilises peptide or corresp, nucleic acid which decreases association of PI 3- or 4- kinase with CD4/p561ck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                        New DNA sequences of s-genes encoding s-proteins - useful for controlling self-incompatibility reaction in self-incompatible plants and s-proteins are gametocides etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD4; T cell; surface antigen; receptor; MHC class II antigen; protein-tyrosine kinase; p561ck; TcR/CD3 complex; PI 3-kinase; PI 4-kinase; lipid kinase; T cell receptor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 8; Length 15;
Pred. No. 1.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 28; 46pp; English.
                                                                                                                          Disclosure; Fig 4; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4 cytoplasmic domain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R60988 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rudd CE;
                                                                                                                                                                                                                                                                                                                                                                                                                      32.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US01840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kanteti P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-293868/36.
    WPI; 1987-137534/20
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                            15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |||||
10 qxprsf 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 QSPRSF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9418832-A
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                                                                                                                                                                                                                                                                                                                        and N70220.
                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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clonal cells from bioactive fractions. Peptides V1320 (gliadin derived peptide) and V1321 (glutenin derived peptide) were identified using these methods, and can be used in pharmaceuticals/medicinus (vaccines) for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e. celiac disease (CD) or celiac sprue, tropical sprue, childhood food allergies and dermatitis herpetiformis (DH). The peptides are also useful for elimination of a group of gluten-sensitive T-cells, and for generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by immunization of a mammal with the

15 AA;

Sequence

peptide

8888888888888

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cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, disease mallitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including proteins protein (beta-APP), the microtubule associated proteins and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein (GFAP), neurofilament-L, neurofilament-M, neurofilament-E, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p33, B-cell leukemia/lymphoma 2 (bc1-2) proto-oncogene, semaphorin III, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
mutation. The method is used to diagnose age-related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides Y13220-13343 represents gluten derived peptides, and their variants. The specification describes a method to find and characterize peptides that are recognized by an intestinally derived gluten-sensitive T-cells. The method comprises establishing and contacting at least one gluten-sensitive T-cell clone with a mixture of gluten-derived peptides, and fractionating the mixture to select peptides that stimulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigenic peptides of gluten and methods for isolating them, useful as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac disease ({\tt CD})
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; wccChe; gluten tolerance; gluten-sensitivity; cellac disease; CD; cellac sprue; tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Naturally occurring variant of the glutenin epitope Y13221,
                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 19; Length 13;
Pred. No. 2.4e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kooy-Winkelaar EMC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 46; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y13338 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                     31.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97EP-0202909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97EP-0202909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 66.7
انتخم 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drijfhout JW, Koning F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-192792/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QSPRSFQKK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 qscrlfkkk 13
                                                                                                                                                                                                                                                                                                                                             13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP905518-A1
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                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y13338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R70619 is a peptide fragment derived from an HIV (Human Immunvalviticiency Virus) protein and is capable of binding to a human lymphocyte antigen. The peptide can induce killer cells which target HIV-intected rells. It is also useful in the prevention and treatment of HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may incorporate devector (such as vaccinia or BCG) contg. DNA encoding the peptides.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-binding peptide fragments from HIV proteins - induce killed cells which target HIV-infected cells and can be incorporated enti-HIV vaccines
                                                                                                                                                                                                                                                                 HLA; human lymphocyte antigen; HIV; human immunodeficiency virus; binding peptide; induce killer cell; prevention; treatment; AIDS;
                              .;
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 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
Score 26; DB 20; Length 15
Pred. No. 2.7e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                       HIV(B35)ARV2-39, human immunodeficiency virus epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 16; L
Pred. No. 2.1e+05;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                              autoimmune disease syndrome; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 11; 61pp; Japanese.
                                                                                                                                                      R70619 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.8%;
62.5%;
 31.0%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       94WO-JP01756.
                                                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0261302.
                                                                                                                                                                                                           14-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miwa K, Takiguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-170188/22.
Query Match
Best Local Similarity
Matches 4; Conserv
                                                      4 ENQSPRSFQK 13
                                                                                3 ggggprgwgg 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
                                                                                                                                                                                                                                                                                                                                                   W09511255-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                             27-APR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                   R70619;
                                                                                                                            RESULT 15
                                                                                                                                          R70619
                                                                                  g
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Search completed: January 17, 2001, 13:36:41 Job time: 116 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 17, 2001, 13:35:50 ; Search time 20.45 Seconds (without alignments) 53.125 Million cell updates/sec Run on:

US-08-765-837-2 84 1 DEDENQSPRSFQKKTR 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues Searched:

2778 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

cripti	1	stylar glycoprotei	scotophobin - rat	tubulin beta-3 cha	cytochrome.c oxida	T-cell receptor be	carboxypeptidase B	heat shock protein	neurotensin - quin	dir	fibrinogen alpha c	protein 0F200022 -	ICL3 protein - Par	insulin-like growt	matrix metalloprot	nifS protein - Bra	Ig kappa chain V-I	T-cell antigen rec	DNA-binding protei	-	ribonucleoside-dip	ribosomal protein	beta-tubulin germ-	T-cell receptor be		T-cell receptor be	Iq heavy chain CRD	P element, P cytot	aspartate transami	tocopherol-binding
SUMMARIES		PQ0193	SFRT	A39703	S65387	PH0756	A26212	S70721	A53608	S68095	JP0101	PA0058	S71300	JH0517	S71948	S04875	F61458	S47376	B34135	146512	A17340	836889	A43839	C36198	PH0772	F49039	PT0281	A39892	A14683	S29272
DB	:	7	٦	~	7	N	N	~	~	~	~	7	7	7	7	~	7	7	~	~	~	~	~	7	7	7	~	~	~	~
Length		15	15	14	10	13	15	10	13	14	15	15	1.5	16	10	11	13	13	14	15	15	15	15	15	15	16	5	ω	80	σ
å Query Match		\sim	8.6	9.8	7.4	7.4	7.4		5.0	5.0		5.0								23.8								5.6		
* O ₩	:	m	7	Ñ	7	~	~	CA	N	(~3	CAI	C	N	CA	CA	CN	CV	(4	CA	N	N	C	CA	C	(4	CA	N	CAI	C	~
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Result No.		7	7	e	7	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT

Scotophobin - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Spate: 23-0ct-1981 #sequence_revision 23-0ct-1981 #text_change 07-Mny-1999
C.Accession: A93164; A92777; A01423
R.Ungar, G.: Desiderio, D.M.; Parr, W.
A.Title: Isolation, identification and synthesis of a specific-behaviour-inducing bra
A.Reference number: A93164; MUID:72240741
A.Reference number: A93164
A.Residues: 1-15 cUNG>
A.Residu

Treell receptor at	zinc-metalLophosph	phospholipase C-be	homeotic protein c	cob protein - comm	T-cell receptor be	calsequestrin, fas	calpain (EC 3.4.22	phyllomedulin - tw	trpE protein - Bac	Rhesus blood group	protein disulfide-	stylar glycoprotei	protein 0F200044 -	T-cell receptor al	light-harvesting p
\$23373	S48209	B48047	S05703	S22040	PH0749	B39040	539392	S07202	I40032	154193	S62620	PQ0192	PA0086	PH1443	D54226
0	~	~	~	7	7	N	~	~	ď	~	7	7	~	~	7
11	12	15	16	16	16	7	10	10	10	11	15	15	15	15	15
22.6	22.6	22.6	22.6	22.6	22.6	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4
19	19	19	19	19	19	18	18	18	18	18	18	18	18	18	18
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

A P P C C C C K P B B B B B B B B B B B B B B B B B B	PRESULT 1 PQ0193 stylar glycoprotein 3 - Peruvian tomato (fragment) N.Alternate names: S3-glycoprotein N.Alternate names: S3-glycoprotein C;Specias: Lycopersicon peruvianum (Peruvian tomato) C;Accession: P00193; A28819 C;Accession: P00193 C;Accession: P00193 C;Accession: P00193 C;Accession: A.; Atlines A.; Anderson, M.A.; Cornish, E.C.; Greyo, B.; Planta 169, 184-191, 1986 A;Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with ex
CAAAAAAAACC	A; Molecule type: protein A; Residues: 1-15 cMAD. A; Repermental Source: style, strain Mill R; Anderson, M. A.; Cornish, E.C.; Mau, S.L.; Williams, E.G.; Hoggart, R.; Atkinson, A. A; T. Crawford, R.J.; Clarke, A.E. A; T. Let 321, 38-44, 1986 A; T. Let a. 21, 38-44, 1986 A; T. Let c. Cloning of cDNA for a stylar glycoprotein associated with expression of sell A; Reference number: A28819 A; Residues: 1-15 cAND> C; Reywords: glycoprotein
λ λ α	Query Match 32.1%; Score 27; DB 2; Length 15; Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 6 QSPRSF 11 1 1111

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A; Accession: S65387
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-10 < SCH>
A; Residues: preliminary
A; Molecule type: protein
B; Residues: 1-10 < SCSCH>
C; Keywords: cardiac muscle; heart; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Local 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-15 <REE>
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                       10 SFQKKT 15
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5 DGNQAP 10
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1 SHQKKT 6
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3 TPRSF 7
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
C;Accession: 865887; 865886
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
R;Schaegger, H.; Noack, H.; 1995
A;Fille: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term A;Reference number: 865372; MUID:95324529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rialexander, J.E.; Hunt, D.F.; Lee, M.K.; Shabanowitz, J.; Michel, H.; Berlin, S.C.; Mac Proc. Natl. Acad. Sci. U.S.A. 88, 4665-4689, 1991
Affilie: Characterization of posttranslational modifications in neuron-specific class II A; Reference number: A39703; MUID:91271258
           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comparison with other neuropeptides; author presents scotophobin sequence in the
    A:Title: The use of mass spectrometry in the structural elucidation of scotophobin -- A;Reference number: A92757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 18-Jun-1993
C;Accession: A39703
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                                                                                                                                A; Note: the sequence was determined by mass spectrometry
R; Stewart, W.W.
Nature 238, 202-209, 1972
A; Title: Comments on the chemistry of scotophobin.
A; Reference number: A91165; WUID: 72240742
A; Contents: annotation; referee's comments on first reference above
R; Ungar, G; Desiderio, D.M.; Parr, W.
Nature 238, 209-210, 1972
A; Reference number: A91166
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: scotophobin
C;Keywords: amidated carboxyl end
F;15/Modified site: amidated carboxyl end (Tyr) #status experimental
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Pred. No. 4.4e+02;
2; Mismatches 4;
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Pred. No. 6e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Scotophobin resurrected as a neuropeptide.
A;Reference number: A43076; MUID:86175024
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Best Local Similarity 45.5.
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                                                                     A;Molecule type: protein
A;Residues: 1-15 <DES>
A;Experimental source: brain
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Nature 320, 313-314, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <ALE>
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Best Local Similarity
Matches 4; Conserv
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EESEAQGPK 14
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T-cell receptor beta chain (I7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: I7-u1-1992 #sequence_revision 17-Ju1-1992 #text_change 05-\psivv-1999
C;Accession: PH0756
C;Accession: PH0756
B;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility compleallelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846
A;Accession: PH0756
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C;Species: Protopterus aethiopicus (marbled lungfish)
C;Species: 10-Sep-1987 #sequence_revision 10-Sep-1987 #text_change 28-Apr-1993
C;Accession: A26212
B;Reference number: 1, 3947-3955, 1972
Biochemistry 11, 3947-3955, 1972
A;Title: Isolation and characterization of pancreatic procarboxypeptidase B and carbo A;Reference number: A90363; MUID:73025047
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A;Residues: 1-13 <CAS>
A;Cross-references: EMBL:X60850; NID:g51482; PIDN:CAA43241.1; PID:g51483
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor
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Score 23; DB 2; Length 10;
Pred. No. 6.2e+02;
0; Mismatches 1; Indels
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80.0%; Pred. No. 9.5e+02;
iive 1; Mismatches 0
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   27.4%;
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R.Min, Y.; Ping, Z.; Yaoshi, Z.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 28, 31-35, 1985
A.Title: Purification and primary structures of duck fibrinopeptides A and B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICL3 protein - Paramecium tetraurella (fragment)
C;Species: Paramecium tetraurella
C;Species: Paramecium tetraurella
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dcc-1999
C;Accession: S71300
R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Bur. J. Blochem. 238, 121-128, 1996
A;Fitle: Characterization of centrin genes in Paramecium.
A;Reference number: S71298; MUID:96248429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Fusarium sporotrichioides
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #fcxt_change 06-Jun-1997
C.Accession: PA0058
R.Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
Submitted to JIPLD, October 1994
A.Reference number: PA0051
                                                                                                                                                                                                               fibrinogen alpha chain - duck (fragment)
N;Contains: fibrinopeptide A
C;Species: Anas platyrhynchos (domestic duck)
C;Species: 30-Jun-1987 #sequence_revision 28-Dec-1987 #text_clange 26-Jan-19.44
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C; Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology C; Superfamily: blood coagulation; plasma; pyroglutamic acid C; Reywords: blood coagulation; plasma; pyroglutamic acid F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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Pred. No. 2e+03;
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Pred. No. 2e+03;
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80.0%;
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57.1%;
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Best Local Similarity 80.vv
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  Conservative
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A;Accession: JP0101
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A; Molecule type: protein
A; Residues: 1-15 <CHO>
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Best Local Similarity
Matches 4; Conserv
                                               1 DEDENQSPRS 10
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6 ETEXQAP 12
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6 SFOKE 10
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C;Species: Orchestia cavimana
C;Date: 21-Apr-1997 #sequence_revision 21-Apr-1997 #text_change 29-Aug-1997
C;Date: 21-Apr-1997 #sequence_revision 21-Apr-1997 #text_change 29-Aug-1997
C;Accession: 868095
Bjochim. Bjophys. Acta 1293, 272-276, 1996
Bjochim. Bjophys. Acta 1293, 272-276, 1996
A;Title: Characterization and N-terminal sequencing of a calcium binding protein from the A;Reference number: 568095; MUID:96202045
A;Accession: 868095
                                                                                                           C; Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998 C; Accession: S70721 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998 C; Accession: S70721 #sequence_revision 17. S23-531, 1995 Mol. Microbiol. 17, 523-531, 1995 A; Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophi A; Reference number: S70719; MUID:96100451
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C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Sep-2000
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C;Keywords: neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                             protein C62.5 homolog - Salmonella typhimurium (fragment) a names: high temperature protein G
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R;Shaw, C.; Thim, L.; Conlon, J.M.
R;Shaw, C.; Thim, L.; Conlon, J.M.
A;Title: [Ser(7)]neurotensin: isolation from guinea pig intestine.
A;Reference number: A53608; MuID:86248085
A;Accession: A53608
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                                                                                                                                                                                                                                                                                A; Modecule type: protein
A; Residues: 1-10 <QIS>
A; Experimental source: strain SL1344
C; Keywords: ATP binding; heat shock; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 2; I Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                          heat shock protein C62.5 homolog -N.Alternate names: high temperatur C.Species: Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%;
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Best Local Similarity 44.4.
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A; Residues: 1-14 <LUQ>
C; Keywords: calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <SHA>
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Best Local Similarity
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Gaps

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Length 11;

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A;Accession: S04875
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-11 <EBBA
A;Cross-references: EMBL:X13691; NID:g39544; PIDN:CAA31982.1; PID:g580775
Genetics:
A;Gene: nifs
A;Start codon: GTG
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Pred. No. 2.2e+03;
2; Mismatches 0; Indels
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Best Local Similarity 60.0%;
Matches 3; Conservative
  A; Reference number: $04873
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3 ENRAP
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R; Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
R) Edochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A; Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth; Reference number: JH0515; MUID: 92109718
A; Accession: JH0517
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Natternate names: MMP-3 protein; stromelysin precursor MMP-3
C; Species: Bos primigenius taurus (cattle)
C; Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C; Accession: 571948
R; Arner, E.C.; Pratta, M.A.; Freimark, B.; Lischwe, M.; Trzaskos, J.M.; Magolda, R.L.; W Biochem. J. 318, 417-444, 1996
A; Article: Isothiazolones interfere with normal matrix metalloproteinase activation and in A; Reference number: 571948; MUID:96404887
A; Molecule type: protein
A; Residues: 1-5;6-10 cARN>
C; Punction:
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A;Note: may be involved in arthritis formation
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nifS protein - Bradyrhizobium japonicum (fragment)
C;Species: Bradyrhizobium japonicum
C;Species: Bradyrhizobium japonicum
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S04875
R;Ebeling, S.
submitted to the EMBL Data Library, December 1988
                                                                                                                      Gaps
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                                                                  Score 21; DB 2; Length 15; Pred. No. 2e+03;
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Pred. No. 2.2e+03;
2; Mismatches 8; Indels
                                                                                                                 1; Indels
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37.5%;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 37.5
Matches 6; Conservative
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Matches 3; Conservative
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A; Residues: 1-16 <COL>
A; Experimental source: serum
                                                                                                                                                             7 SPRSFQK 13
A; Genetic code: SGC5
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1 APQSAQK 7
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

January 17, 2001, 13:36:45; Search time 12.32 Seconds (without alignments) 41.940 Million cell updates/sec

US-08-765-837-2 84 1 DEDENQSPRSFQKKTR 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 seqs, 32294092 residues Searched:

111 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	P01159 rattus norv	P81018 oncorhynchu	Q56715 vibrio prot	rattus	Q56251 tomato big	P19628 protopterus	P14630 rattus norv	P32560 cavia porce		P24854 sus scrofa	P56575 rattus norv	P37030 bradyrhizob		P24927 albizzia ju	homo sapi	_	P08610 phyllomedus	Q44160 prunus arme		Q46490 clover yell				_	-	P22395 locusta mig	_	P41490 locusta mig	P43669 salmonella		P16392 equus cabal	56870 rhodococ	P42052 cucumis sat
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16 1 TRYP_FELCA 16 1 YMOR_PSEPU 8 1 ALL3_CARMA 8 1 ALL4_CALVO 8 1 ALL4_CALVO 8 1 ALL4_CYDPO 8 1 B44K_PORGI 8 1 FAR3_HOMAM 9 1 FARP_CALSI 10 1 XYNB_DICB4 11 1 TKNA_ONCMY	PLT 1 SCOT_RAT STANDARD; PRT; 15 AA. P01159; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1998 (Rel. 01, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) 15-JUL-1998 (Rel. 36, Last annotation update) 15-JUL-1998 (Rel. 36, Last annotation update) SCOTOPHOBIN. Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; SEQUENCE, AND SYNTHESIS. MEDLINE-72240741; PubMed-4558348; Inducing brain peptide."; Nature 238:198-202(1972). [2] SEQUENCE. Desiderio D.M., Ungar G., White P.A.; J. Chem. SCC. Chem. Commun. 432-433(1971). [3] [3] [4] SEPERES COMMENTS ON REF. 1. MEDLINE-72240742; PubMed-4558349; Stewart W.W.; "Comments on the chemistry of scotophobin."; Nature 238:202-209(1972). [4] Nature 238:202-209(1972). [5] Nature 238:202-210(1972). [6] Nature 238:202-210(1972). [7] Nature 238:203-210(1972). [8] Nature 238:203-210(1972). [8] Nature 238:203-210(1972). [8] Nature 238:208-8PECTFICITY: BRAIN. Amidation. MOD_RES. SEQUENCE 15 AA: 1582 MW; 5B87696F6C7FD76C CRC64;	arity 45.5%; Pred. No. 1.7e+02 onservative 2; Mismatches FOK 13 : AQQ 12 STANDARD; PRT; 11 AA. Rel. 35, Created) Rel. 35, Last sequence update) Rel. 37, Last annotation update) (FRAGMENT).
19.0 17.9 17.9 17.9 17.9 17.9 17.9 17.9 17.9	AT STANK 1986 (Rel. 01 1996 (Rel. 01 1999 (Rel. 36 HOBIN DOLVOSICUS (F CC. AND SYNTHE E=72240741; Pu CG. Desiderio Tio D.M., Unge Ti	PO P
166 115 115 115 115 115 115	SCOT RAT STANDARD; 201-701-1986 (Rel. 01, Cr 21-JUL-1986 (Rel. 01, Le 15-JUL-1998 (Rel. 01, Le 18-JUL-1998 (Rel. 01, Le 19-JUL-1998 (Rel. 01, Le 1	
00000000000000000000000000000000000000	RESULT SCOT_RAT ID SCOT SCOT SCOT SCOT SCOT SCOT SCOT SCOT	Query Mat Best Loca Matches Qy 3 1 Db 2 1 LADD_ONCMY 1D LADD_C AC P81018 AC P81018 DT 01-NOV DT 01-NOV DT 01-NOV DT 01-NOV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97143305; PubMed-8996113;
Setterquist R.A., Smith G.K., Oakley T.H., Lee Y.H., Fox G.E.;
Setterquist R.A., Smith G.K., Oakley T.H., Lee Y.H., Fox G.E.;
Sequence, Overproduction and purification of Vibrio proteolyticus ribosomal protein L18 for in vitro and in vivo studies.";
Gene 183:237-242(1996).
-! FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS LOCATED AT THE ANIVOACYL-TRNA BINDING SITE OF THE PEPPIDYLTRANSFERASE CENTER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio proteolyticus (Aeromonas proteolytica).
Bacteria: Proteobacteria: gamma subdivision; Vibrionaceae; Vibrio.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                 0;
                                                                                                              Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
"A rainbow trout lectin with multimeric structure.";
Comp. Biochem. Physiol. 116B:385-390(1997).
-!- FUNCTION: LECTIN THAT BINDS SEPHAROSE.
-!- COFACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.
-!- SUBUNIT: MULTIMERIC.
                                                                                                                                                                                                                                                                                    Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 1; Length 16;
Pred. No. 2.6e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                Score 24; DB 1; Length 11;
Pred. No. 1.7e+02;
L; Mismatches 2; Indels
                                                                                                                                                                                                                                       OB26227FF6D45404 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
50S RIBOSOMAL PROTEIN L6 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00525; RIBOSOMAL_L6_1; PARTIAL. Ribosomal protein; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                 MEDLINE-97293418; PubMed-9149391; MEDLINE-97293418; PubMed-9149391;
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15-DEC-1998 (Rel. 37, Last sequ
15-DEC-1998 (Rel. 37, Last and
                                                                                                                                                                                                                                                                                  28.6%;
57.1%;
                                                                                                                                                                                                                                       11 AA; 1163 MW;
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41.7%;
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Best Local Similarity 41.7
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserv
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Q56715;
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-!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S199 FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                      Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.; "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.";
                                                                                                                                                                               Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Biochem. 230:235-241(1995).
-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CALAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.: "Phylogeny of mycoplasmalike organisms (phytoplasmas): a basis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VIIB (EC 1.9.3.1) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA; 1210 MW; CFC70EB771A33326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 1; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30S RIBOSOMAL PROTEIN S19 (FRAGMENT)
RPSS OR RPS19.
                                                                                                                                                                                                                                                                                                          MEDLINE-95324529; PubMed-7601105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94350802; PubMed=8071198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomato big bud phytoplasma.
Bacteria; Firmicutes; Bacillus/C
Acholeplasmataceae; Phytoplasma
                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
01-FEB-1996 (Rel. 33, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Mitochondrion.
NON_TER 10 10
                                                                                                                                                                                                                                                                                    STRAIN-WISTAR; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%;
STANDARD;
                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 FERRICYTOCHROME C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        their classification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SHQKKT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RS19_TOBBP
COXM_RAT P80431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
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Gaps

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DENOSPRSFORK 14

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"A novel high-density lipoprotein particle and associated protein in
                                                                    rat plasma.";
Blochim. Biophys. Acta 1042:19-27(1990).
-!- FUNCTION: UNKNOWN.
-!- TISSUE SPECIFICITY: PLASMA PROTEIN ASSOCIATED WITH
                      MEDLINE-90122905; Pubmed-2297521;
Blatter M.-C., James R.W., Borghini I., Martin B.M.,
Hochstrasser A.-C., Pometta D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
13 AA; 1680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                    Local Similarity 45.5
les 5; Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                      5 NOSPRSFOKKT 15
                                                                                                                                                                                                                                             4 NOXPEXSOLTT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRINOPEPTIDE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ENQSPRSF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasma; HDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBA_ANAPL
P12801;
                                                                                                                                                                                                                                                                                                     NEUT_CAVPO
P32560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vasoactive.
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              SEOUENCE.
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NEUT_CAVPO
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14; ALSO KNOWN AS THE ZINC CARBOXYPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Dipnoi, Lepidosireniformes, Protopteridae, Protopterus.
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0
                                                                                                                 Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                      4; Indels
                                                                   NON_TER 1 1 1
SEQUENCE 12 AA; 1470 MW; 4CC88BE908333AA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124C910D937BED65 CRC64;
                                                                                                              Score 23; DB 1; I
Pred. No. 2.8e+02;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; I
Pred. No. 3.6e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
CARBOXYPEPTIDASE B (EC 3.4.17.2) (FRAGMENT).
Protopterus aethiopicus (Marbled lungfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PX_RAT STANDARD; PRT; 16 AA. P14630; 01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update) PROTEIN PX (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO, IPRO00834; -
PROSITE; PRO0132; CARBOXYPEPT_ZN_1; PARTIAL.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; PARTIAL.
Hydrolase; Carboxypeptidase; Zinc; Zymogen.
                                                                                                                                                                                                                                             15 AA.
                               INTERPRO; IPR002222; -: PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL RIBOSOMAl protein; rRNA-binding.
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             PRT;
                                                                                                              27.4%;
40.0%;
                    EMBL; L27004; AAA83952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 15
15 AA; 1749 MW;
                                                                                                                            Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.4
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-LYSINE/ARGININE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A26212; A26212.
MEROPS; M14.003; -.
                                                                                                                                                                           1: : | | |
3 NKKDKKMQKK 12
                                                                                                                                                             5 NQSPRSFQKK 14
                                                                                                                                                                                                                                                                                                                                                                          TISSUE-PANCREAS;
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3 TPRSF 7
                                                                                                                                                                                                                                            CBPB_PROAT P19628;
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SEQUENCE
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
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CBPB_PROAT
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SORRERE
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                                                                                                                                     Caps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
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MEDLINE=86748085; PubMed=3087775;

Shaw C., Thim L., Conlon J.M.;

"[Ser7]neurotensin: isolation from guinea pig intestine.";

"ESES Lett. 202:187-193(1986).

-!- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.

PIR; A53608; A53608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 1; Length 13; Pred. No. 6.5e+02; 2; Mismatches 2; Indels
                                                                                      27.4%; Score 23; DB 1; Length 16; 45.5%; Pred. No. 3.8e+02;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
4C8314644C4115B3 CRC64;
NON_TER 16 16 18
SEQUENCE 16 AA; 1740 MW; 79836ECDAE9FBA29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
NEUROTENSIN (NT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            13 AA.
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                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE-85168193; PubMed-3983613;
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1 DEAIHXPPPSEEKLAR 16

Yaoshi Z.;

Min Y.,

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(Rel.
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1 QERRQSP 7
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01-JUN-1994
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                                                                                                                                   UH09_RAT
P56575;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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0
                                                                             Sci. Sin., B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                              (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANBOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
BLOOD COAGULATION; Plasma.
MOD PRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92109718; PubMed-1722398;
Coleman M.E., Pan Y.-C.E., Etherton T.D.;
Coleman M.E., Pan Y.-C.E., Etherton T.D.;
Identification and NH2-terminal amino acid sequence of three "Identification and NH2-terminal amino acid sequence of three insulin-like growth factor-binding proteins in porcine serum.";
Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
-!- FUNCTION: IGP-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                      "Purification and primary structures of duck fibrinopeptides A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: SECRETED.
-1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
-1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
11SSLIN-LIKE GROWIF FACTOR BINDING PROTEIN 4 (IGFBP-4) (IBP-4)
(IGF-BINDING PROTEIN 4) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                          AGGREGATION.
-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 1; Length 15;
Pred. No. 7.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D78A51FF88B40373 CRC64;
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PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
Growth factor binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AA; 1580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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PIR; JH0517; JH0517.
INTERPRO; IPR000716; -.
INTERPRO; IPR000867; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFOKE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBP4_PIG
ID IBP4_PIG
AC P24854;
                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
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SEQUENCE
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SEQUENCE.
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                                                                                                                                                                                                                              STRAIN=WISTAR; TISSUE=HEART;
Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
Jungblut P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                          Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                         Submitted (SEP-1998) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
-- PROTEIN IS: 8.9, ITS MW IS: 42 KDA.

NON_TER 8
                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P9) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 1; Length 8; Pred. No. 8.9e+04; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ebeling S.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NOT KNOWN YET.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09F0BB69476DC404 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;
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PIR; SO4875; SO4875.
PIREPRO, 1PR000192; -
PROSITE; PS00595; AA_TRANSFER_CLASS_5; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
8 AA.
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(Rel. 29, Last sequence update)
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NON_TER 11 11
SEQUENCE 11 AA; 1308 MW; 09F0BB6947
PRT;
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Matches 3; Conservative
STANDARD;
                                                                                                                        Rattus norvegicus (Rat).
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53165F7E9C45B4D0 CRC64;

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Serine protease inhibitor.
NON_TER 15 15
SEQUENCE 15 AA; 1705 MW;
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UPA1_HUMAN
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MEDLINE-97385165; PubMed-9238039;
Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
Afamily of fibrinogen-related proteins that precipitates parasitederived molecules is produced by an invertebrate after infection.";
Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).
--I-FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
ECHINOSTOMA PARABNESI.
--I-SUBCELLULAR LOCATION. SECRETED IN THE HEMOLYMPH.
                                                                                                                                                                                                                                   Biomphalaria glabrata (Bloodfluke planorb).
Eukaryota: Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Planorbidae; Biomphalaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-80115605; PubMed=528539;
Odani S., Ono T., Ikenaka T.;
Proctainase inhibitors from a mimosoideae legume, Albizzia
"proctainase inhibitors from a mimosoideae legume, Albizzia
julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
J. Biochem. 86:1795-1805(1979).
-!- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
-!- FUNCTION: TERRODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
DISULFIDE BOND.
-!- SIMILARITY: TO BETA CHAINS OF SOME OTHER LEGUMINOUS KUNITZ-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Albizzia julibrissin (Silk tree).
Wakaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Mimosoideae; Albizia.
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 Score 20; DB 1; Length 11;
Pred. No. 7.9e+02;
2; Mismatches 0; Indels
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16 16
16 AA; 1964 MW; A1665754589EF82C CRC64;
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01-OCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
HEMOLYMPH 65 KDA LECTIN BG06 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
TRYPSIN INHIBITOR B CHAIN (FRAGMENT).
                                                                                                                                             16 AA.
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23.8%;
60.0%;
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ilarity 42.9%;
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Best Local Similarity
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ID LE06_BIOGL
AC P80745;
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P24927;
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Electrophoresis 13:707-714(1992).
--- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.9, ITS MW IS: 65 KDA.
SWISS-2DPAGE; P30087; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 1; Length 8;
Pred. No. 8.9e+04;
2; Mismatches 3; Indels
                       Length 15;
                                                                    Indels
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                  Score 19; DB 1; Le
Pred. No. 1.6e+03;
1; Mismatches 0;
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Job time: 163 sec
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Best Local Similarity 37.5%;
Matches 3; Conservative
                       22.6%;
75.0%;
Query Match
Best Local Similarity 75.0.
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081784 hepatitis c
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081787 hepatitis c
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MEDLINE=91139577; PubMed=1995588;
Tao T., Bourne J.C., Blumenthal R.M.;
Ta family of regulatory genes associated with type II restriction:
modification systems.",
J. Bacteriol. 173:1367-1375(1991).
                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria; proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
LIGHT-CHAIN COMPLEMETARITY-DETERMINING REGION 3 MRNA (CLONE 14),
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Last annotation update)
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Pred. No. 5.3;
1; Mismatches
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
Query Match
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Matches 7; Conserv
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SEQUENCE
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Q47603;
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066190 avian infec
063940 rattus norv
093107 mesocricetu
035411 mus musculu
093166 rattus norv
097674 homo sapien
095810 gallus gall
095817 pinus conto
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Q83960 influenza a
Q67605 squash leaf
Q67606 squash leaf
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                                                     Search time 32.75 Seconds
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(c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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sp_phage:*
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Result

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Gaps

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Rattus norvėgicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                            Niesters H.G., Lenstra J.A., Spaan W.J., Zijderveld A.J., Bleumink-Pluym N.M., Hong F., van Scharrenburg G.J., Horzinek P.C., der Zeijst B.A., The peplomer protein sequence of the M41 strain of coronavirus IBV and its comparison with Beaudette strains."; virus Res. 5.253-263(1986).

EMBL, M21883, AAA66576.1; -.
                  Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
03-0CT-2000 (TrEMBLrel. 15, Last annotation update)
P53 TUMOR SUPPRESSOR (FRAGMENT).
Mesocricetus auratus (Golden hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-94140941; PubMed-8308072;
Morgan M.J., Earnshaw J.C., Dhoot G.K.;
"Novel developmentally regulated exon identified in the rat fast
skeletal muscle troponin T gene.";
J. Cell Sci. 106:903-908(1993).
EMBL; S68786; CAB32909.1; -
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Pred. No. 5.7e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                            NON_TER 10 10 SEQUENCE 10 AA; CF2510D5A1B775A6 CRC64;
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Last annotation update)
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 avian infectious bronchitis virus
                                                                                                              STRAIN=41;
MEDLINE=87021475; PubMed=2429473;
                                                                                                                                                                                                                                                                                                                                                                   29.8%;
83.3%;
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50.0%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                           SEQUENCE FROM N.A.
                                                        NCBI_TaxID=11120;
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Q63940;
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                                                                                      SEQUENCE FROM N.A.
MEDLINE-92052225; PubMed=1719545;
Burton D.R., Barbas C.F. III, Persson M.A., Koenig S., Chanock R.M.,
Lerner R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                       "A large array of human monoclonal antibodies to type 1 human immunodeficiency virus from combinatorial libraries of asymptomatic seropositive individuals.";

ENDL, MAGAG, Sci. U.S.A. 88:10134-10137(1991).

EMBL, M80720; AAA44780.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burton D.R., Barbas C.F. III, Persson M.A., Koenig S., Chanock R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A large array of human monoclonal antibodies to type 1 human immunodeficiency virus from combinatorial libraries of asymptomatic seropositive individuals.";

Puroc. Natl. Acad. Sci. U.S.A. 88:10134-10137(1991).

EMBL; M80726; AAA44786.1; -.
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pred. No. 4.7e+02;
2; Mismatches 1; Indels
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Pred. No. 4.7e+02;
2; Mismatches 1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
LIGHT-CHAIN COMPLEMETARITY-DETERMINING REGION 3 MRNA
                                                                                                                                                                                                                                                                                                             16 AA; 1883 MW; 9015605C32B3D65E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9015605C32B3D65E CRC64;
             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLONE 31), PARTIAL CDS (FRAGMENT).

Human immunodeficiency virus type 1.

Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA.
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57.1%;
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57.1%;
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Best Local Similarity 5/...
Best Local 4; Conservative
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PARTIAL CDS (FRAGMENT).
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Best Local Similarity
Matches 4; Conserv
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7 NSAPRTF 13
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7 NSAPRTF 13
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Q79461;
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Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostani;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99276463; PubMed-10343117;
Graphodatsky A.S., Vorobieva N.V., Filipenko M.L., Voronina E.V.,
Frengen E., Prydz H.;
"Assignment of the Lil ribosomal protein gene (RPLI1) to human
chromosome 1p36.1->p35 by in situ hybridization.";
Cytogenet. Cell Genet. 84:97-98(1999).
EMBL; AF101385; AAD20460.1;
EMBL, AF101384: AAD20460.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MG-ATPASE 85 KDA GLYCOPROTEIN COMPONENT (EC 3.6.1.3) (FRAGMEHT).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 4; Length 13;
Pred. No. 1.9e+03;
3; Mismatches 2; Indels
EMBL; AF189711; AAF26304.1; -.
NON_TER 11 11
SEQUENCE 11 AA; 1255 MW; 804D1A1E6DDAA325 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
RIBOSOMAL PROTEIN L11 (FRAGMENT).
                                                                                          Score 23; DB 11; L
Pred. No. 1.1e+03;
3; Mismatches 3;
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                                                                                            27.4%;
33.3%;
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Best Local Similarity 37.5%;
Matches 3; Conservative
                                                                                        Query Match 27.4 Best Local Similarity 33.3 Matches 3; Conservative
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4 DQGEKENP 11
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SEQUENCE
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Q9PS10;
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                                                                                        Laverdiere M., Beaudoin J., Lavigueur A.;
"Speciacs-specific regulation of alternative splicing in the C-terminal region of the p53 tumor suppressor gene.";
Nucleic Acids Res. 28:1489-1497(2000).
BMBL: AF190271; AAF4379-1; -.
SEQUENCE 8 AA; 969 MW; 1DB6D9CDC41761E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rundlof A.-K., Arner E.S.J.; "Genomic sequence of parts of the rat thioredoxin reductase 1 gene."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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TSG W.T., Peters L.L., John K.M., Lux S.E.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, AR026489; AAC79505.1; -...

MGD; MGI:1313261; Spb3.
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01-CCT-2000 (TrEMBLrel. 15, Created)
1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
THIOREDOXIN REDUCTASE (FRAGMENT).
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Last annotation update)
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40.0%;
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Similarity 80.0%;
4; Conservative
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Matches 4; Conserv
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                    NCBI_TaxID=10036;
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                                                                       TISSUE-KIDNEY;
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3 PRAFQ 7
   Mesocricetus
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Spinacia oleracea (Spinach).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Caryophyllales; Chenopodiaceae; Spinacia.

NCBI_TaxID=3562;
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Mammalia; Eutheria; Rodentia; Hystricognathi; Cavlidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS. INTERPRO; IPR001848; -. PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
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SEQUENCE 16 AA; 1880 MW; 21844A5F5767CB17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PROTEIN ISOMERASE-RELATED PROTEIN PRECURSOR 71.5 KDA ISOFORM (FRACMENT).
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CHLOROPLAST 30S RIBOSOMAL PROTEIN S10 BETA (FRAGMENT).
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                   Pred. No. 3.4e+03;
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MEDLINE=96070119; PubMed=8535285;
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SEQUENCE 16 AA; 1666 MW; 4B7
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66.7%;
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                 Best Local Similarity 41.7
Matches 5; Conservative
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9 SPDSFE 14
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Dharmawardhana D.P., Ellis B.E., Carlson J.E.;
"A beta-glucosidase from lodgepole pine xylem specific for the lignin
precursor coniferin.";
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Coniferopsida; Coniferales; Pinaceae; Pinus.
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Caryophyllales; Chenopodiaceae; Spinacia
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01-JUN-2000 (TERBLEE]. 14, Last annotation update)
CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 ALPHA (FRAGMENT).
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EQUENCE 16 AA; 1812 MW; A7072AD36067C086 CRC64;
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BETA-GLUCOSIDASE (FRAGMENT).
              80.08;
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ENQRP 15
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Parvin J.D., Young J.F., Palese P.;
Nonsense mutations affecting the lengths of the NS1 nonstructural proteins of influenza A virus isolates.";
Virology 128:512-517(1983).
EMBL; K0962; AAA45316.1; -.
INTERPRO; PIRO00256; -.
INTERPRO; Flu_NS1; 1.
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SEQUENCE 16 AA; 1811 MW; 23F434B5AEEFAD93 CRC64;
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PATENT NO. 5332671

PAPPLICANT: PERRARA, NAPOLEONE; LEUNG, DAVID W.H.

TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL

GROWTH FACTOR AND DNA ENCODING SAME

NUMBER OF SEQUENCES: 15

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/389,722

FILING DATE: 04 -NUG-1989

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM 1.
TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
NUMBER OF SEQUENCES: 58
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,623
FILING DATE: 22-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; Score 35; DB 5; Length 13; 100.0%; Pred. No. 4.7; tive 0; Mismatches 0; Indels
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US-08-541-964-37
US-08-65-647-52
US-08-693-697-17
US-08-693-697-17
US-08-693-697-17
US-08-480-190-186
US-08-480-379-186
US-08-480-379-186
US-08-480-379-186
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FILING DATE: 21-JUN-1989
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FILING DATE: 12-MAY-1989
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SEQ ID NO:10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-94-915-189

US-08-439-818A-11

US-08-738-95-11

US-08-738-95-11

US-08-738-95-11

US-08-738-95-11

US-08-738-95-11

US-08-738-94-11

US-08-73-415B-16

US-09-101-146-14

524706-13

US-08-467-023-246

S196511-24

US-08-467-023-246

S196511-24

US-08-467-023-075-58A-5

US-08-161-105

US-08-161-105

US-08-181-105

US-08-181-105

US-08-181-105

US-08-181-105

US-08-181-105

US-08-181-105

US-08-181-105

US-08-181-105

US-08-181-1205

US-08-181-1205
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             174772 seqs, 17957048 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                   January 17, 2001, 13:35:00
                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                          1 DEDENQSPRSFQKKTR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                    US-08-765-837-2
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                            Sequence:
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0

Caps

0;

Gaps

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Mismatches

Length 13;

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36.9%; Score 31; DB 2; Length 11; 40.0%; Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08317522A
Patent No. 559918
CENERAL INFORMATION:
FURUAR FURUAR, Michiko N.
TITLE OF INVENTION: Prophinin and Trophinin-Assisting
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,522A
FILING DATE: 04-OCT-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                 SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/949,836
FILING DATE: APPLICATION NUMBER: 07/949,836
FILING DATE: APPLICATION NUMBER: 07/338
RECISTRATION NUMBER: 37,133
RECISTRATION NUMBER: 37,133
RECISTRATION NUMBER: 37,133
REPERBNCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELECHOME: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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1 DQDQSQTPET 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                             Sequence 13. Application US/07909122
Patent No. 5415995
GENERAL INFORMATION:
APPLICANT: SCHOOLNIK, GARY K.
APPLICANT: PALEFSKY, JOEL M.
TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA TITLE OF INVENTION: VINUS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 1; Length 11;
Pred. No. 18;
5; Mismatches 1; Indels
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Patent No. 5932412
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: CHENG, HWRE-MIG
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
----ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28600-20105.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REFRENCE/DOCKET NUMBER: 2860
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 494-0792
TELEFX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.9%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                      STREET: 755 Page M
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DEDENQSPRS 10
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1 DQDQSQTPET 10
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US-08-934-915-189
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US-07-909-122-13
                                                             US-07-909-122-13
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Sequence 11, Application US/08738975

Patent No. 5880267

GENERAL INFORMATION:

APPLICANT: Funda, Michiko N.

TITLE OF INVENTION: Trophinin and Trophinin-Assisting

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 30; DB 2; Length 9; 62.5%; Pred. No. 1.3e+05; Live 1; Mismatches 2; Indels
TITLE OF INVENTION: Trophinin and Trophinin-Assisting TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 22
CORRESPONDENCES: ADDRESS: ADDRESSE: Campbell and Flores STRET: 4370 La Jolla Village Drive, Suite 700 CITY: San Diego STATE: California
                                                                                                                                                          STATE:
COUNTRY: USA
ZIP: 92122
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
COMPUTER: LBW PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,965
FTI.ING DATE: HETEWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,975
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EDENQSPR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : ||| ||
1 DQENQDPR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
US-08-751-965-11
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US-08-738-975-11
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                                                                                                                                 Score 30; DB 1; Length 9; Pred. No. 1.3e+05; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08439818A
Patent No. 5654145
GENERAL INFORMATION:
FILLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,818A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 3.1815
REFERENCE/DOCKET NUMBER: P-LA 1563
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPA: (619) 535-801
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   %208-751-965-11

Sequence 11, Application US/08751965

Patent No. 5858360

GENERAL INFORMATION:

APPLICANT: Fukuda, Michiko N.
                                                                                                                                 35.7%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                 Query Match 35.7
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 62.5
Matches 5; Conservative
      LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
                             ; TYPE: amino acid
; TOPOLOGY: linear
US-08-317-522A-11
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US-08-439-818A-11
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1 DQENQDPR 8
                                                                                                                                                                                                                       2 EDENQSPR 9
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1 DQENQDPR 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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Gaps
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TITLE OF INVENTION: Trophinin, Trophinin-Assisting
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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APPLICANT: deLaluna, Susana
TITLE OF INVENTION: TRENSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .3e+05;
es 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILOATION NUMBER: US/08/808,599A
FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                        E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 3;
Pred. No. 1.3e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/317,522
FILING DATE: 04-0CT-1994

PRIOR APPLICATION UNBER: US 08/439,818
APPLICATION UNBER: US 08/439,818
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2256
                                                                                                                                                                     Sequence 11, Application US/08808599A Patent No. 6111089
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-723-415B-16; Sequence 16, Application US/08723415B; Pattent No. 5859199; ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                             GENERAL INFORMATION:
                         2 EDENOSPR 9
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1 DQENQDPR 8
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1 DQENQDPR
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                                                                                                                                               US-08-808-599A-11
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                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fukuda, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
TITLE OF INVENTION: Proteins
FORTHAMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,626
                                                                                                                                                                                                                                                                                                                                      Score 30; DB 2;
Pred. No. 1.3e+05
1; Mismatches
                                      NAME: Campbell, Cathryn A.
REGIGSTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2251
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9849
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION 1973.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LA 1563
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08728626
Patent No. 5910451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   35.7%;
62.5%;
FILING DATE: 05-Dec-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62...
5; Conservative
                                                                                                                                                                                                                                                                                                                                   Query Match 35.7
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                             9 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 4370 La JC
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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1 DQENQDPR 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                          US-08-738-975-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-728-626-11
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us-08-765-837-2.closed.rai

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Query Match 35.7%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DENQSPRSFQK 13
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                         1 DEDENQSPRS 10
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; LENGTH: 11
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US-09-101-146-14
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Sequence 16, Application US/09189627A

Patent No. 6158691

GENERAL INFORMATION:
APPLICANT: La Thanque, Nicholas
APPLICANT: La Thanque, Nicholas
APPLICANT: La TRANSCRIPTION PACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54

CURRENT APPLICATION NUMBER: US/09/189,627A

CURRENT FILING DATE: 1998-11-10

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-30

PRIOR FILING DATE: 1996-09-15

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:DP-3 peptide to ; OTHER INFORMATION: raise antiserum US-09-189-627A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
                                                                                                                    COMPUTER REALIZED CONTOUR MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: PATENTIAN PATE: PATENTIAN DATA: APPLICATION NUMBER: US/08/723,415B FLING DATE: 30-58P-1996 CLASSIECATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9610195.1 FTLING DATE: 15-MAY-1996 ATTORNEY/AGENT INFORMATION: NAME: Crawford, Arthur R. REGISTRATION NUMBER: 25,327 CREMISSION NUMBER: 1117-220
8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 2;
Pred. No. 32;
2; Mismatches
STREET: 1100 No. 5859199th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.7
Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                 ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DEDENQSPRS 10
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2 EEDEEEDPSS 11
                    Arlington
                                                                 USA
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                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                          GENERAL INFORMATION:

APPLICANT: Destrouch College, St. Vincents Institute of
APPLICANT: Medical Research, Kemp et al.

TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
NUMBER OF SEQUENCES: 64
CORRESPONDENCES: Jane Massey Licata, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
5240706-13
; Patent No. 5240706
APPLICANT: FAULDS, DARYL
; TITLE OF INVENTION: INTRANASSAL ADMINISTATION OF MYCOPLASMA; HYOPNEUMONIAE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 3; Length 16;
Pred. No. 40;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
FILLING DATE: OCCODER 7, 1998
CLASSIFICATION DATA:
APPLICATION NUMBER: B 74
RILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                        CITY: Mariton STATE: NJ COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/334,586
FILING DATE: 07-APR-1989
Sequence 14, Application US/09101146 Patent No. 6124125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jane Massey Licata
REGISTRATION UNDHBER: 32,257
REFERENCE/DOCKET UNDHBER: DC-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1151
TELEPAX: (856) 810-1151
INFORMATION FOR SEQ ID NO: 14:
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                                                                                                                                                                                                                                                                                                                                                            WESULI 15

US-08-677-298-16

Sequence 16, Application US/08677298

Patent No. 5863729

GENERAL INFORMATION:

HITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1

TITLE OF INVENTION: LINASE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STRET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STRET: 670 Manhattan Circle, Suite 201

CITY: Boulder

STRET: 670 Manhattan Circle, Suite 201

CITY: Boulder

STREE: 5370 Manhattan Circle, Suite 201

COUNTRY: USA

IP 80303

COMPUTER: EMP PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

COMPUTER: Patentin Release #1.0, Version #1.30

COMPUTER: Jum PC Compatible

OPERATING SYSTEM: DATE: US/08/677,298

FILING DATE: 09-UUL-1996

CLASSIFICATION NUMBER: 34,464

REFERENCE/DOCKET NUMBER: 9-96

TELECOMMUTCATION INFORMATION:

MAME: CATULDEN: 536

ATTORNEY, GASTIENTION: 536

TELECOMUTICATION NUMBER: 9-96

TELECOMUTICAT
Score 29; DB 5; Length 11;
Pred. No. 39;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%; Score 28; DB 2; Length 13; 50.0%; Pred. No. 68; 3; Indels tive 2; Mismatches 3; Indels
34.5%;
83.3%;
Query Match 34.5
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DEDENQSPRS 10
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6 DENQKP 11
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Search completed: January 17, 2001, 13:37:03 Job time: 123 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

January 17, 2001, 13:37:10 ; Search time 14.29 Seconds (without alignments) 23:928 Million cell updates/sec Run on:

US-08-765-837-3 55 1 TDGSFTQPLY 10 Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

268485 segs, 34193795 residues Searched:

74110 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS1/gcqdata/geneseq/geneseqp/AA1991.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:* /SIDSI/goddata/geneseq/geneseqp/AA1996.DAT:*/SIDSI/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDSI/gcgdata/geneseq/geneseqp/AA1998.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:* A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Factor VIII antide	Secretin precursor	Intermediate of Se	Immunodenic per	Rat mACHR-6 transm	Prostate specii	HLA-A1 PSA antiqen	Rheumatoid art	Peptide fragmer	LN clone F11 Vbeta	Immunogenic peptid	20011 GU COMA
	ID	R90947	P20399	P30039	Y45512	W92985	Y38373	R49207	Y41894	R61602	R89241	Y48114	V55202
	DB	17	m	4	20	20	15	15	20	15	17	20	20
	luery Match Length DB	10	10	10	80	∞	10	10	10	10	10	10	v
¢	Query Match	100.0	50.9	50.9	49.1	49.1	49.1	49.1	47.3	43.6	41.8	41.8	40
	Score	55	28	28	27	27	27	27	26	24	23	23	22
	Result No.	1	8	m	4	2	9	7	80	σ	10	11	12

Human harmatonolog	Escherichta coli q	N-terminus of huma	Peptide iragment (Dopamine receptor	Peptide containing	Random peptide seq	Interleukin-1 type	. Mutant hepatitis B	Interleukin-1 type	B 11.646	Ø	N-terminal of anti	Antibody displacin	Rheumatold arthrit	Beta-1 integrin ce	Peptido fragment o	Glutamate dehydrog	Internalisation si	Hexapeptide #1 bin	Sept	ATCC HB 11885 mono	Human haematopoiet	Hybridoma ATCC HB-	ATCC HB 1.1885 mono	Human haematopoiet	Zif268 mutagenised	Human insulin anal	HLA binding plu-1	3	plasmid p-DL6 pept	PMEL	ScFV (dig) variant
Y87039	W70510	X56067	R61553	R93565	W16026	W68664	W58143	Y14118	X09787	Y55114	Y86860	R14205		Y41936	Y28543	R47939	W15410	R41655	W75346	W75278	Y55291	Y87037	R90407	Y55134	Y86880	R83498	W94594	Y55322	38	116	æ	
2	13	21	15	17	18	19	19	20	20	20	21	12	11	20	20	15	18	14	13	19	20	21	17	20	21	16	17	20	20	21	18	20
œ	7	σ			10					9	9	7	8	8	6	10		9	9	9	9	9	7	7	7	80	89	80	80	80	σ	σ
40.0	40.0	40.0		0	40.0	o.	٥.	0	0		8	8	8	8	8	8	8	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	9	36.4	36.4	36.4	36.4	36.4
22	22	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21	21	20	20	20	70	70	20	50	20	20	20	20	20	50	20	20
13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT R90947

R90947 standard; peptide; 10 AA.

R90947;

(first entry) 09-SEP-1996

Factor VIII antigenic peptide corresp. to residues Thr.1739-Tyr1748.

Factor VIII; modification; inhibitor activity; binding; antibody; von Willebrand factor; immune disorder.

WO9602572-A2. Synthetic.

01-FEB-1996

95WO-BE00068 14-JUL-1995; 94BE-0000666. 14-JUL-1994;

(CROI-) CROIX ROUGE BELGIQUE

Laub R; Di Giambattista M,

WPI; 1996-105861/11.

Factor VIII antigenic polypeptide fragments and epitope(s) - also inhibitors of factor VIII and anti-inhibitors, useful for e.g. preventing and treating immune disorders involving inhibition of factor VIII binding

Claim 8; Page 31; 45pp; French.

Gaps

.; 0

Indels

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are useful in the production of this precursor. The precusor is treated with strong acid in the preparation of secretin. Secretin is one of the digestive canal hormones and is useful in promotion of pancreatic external secretin, controlling gastrin-stimulating secretin of the stomach acid, releasing insulia, stimulating secretin and decomposing fat. It is used as a pancreatic-function examining agent and a medicine for curing duodenal ulcers etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The peptide is an industrial intermediate for the production of secretin. Secretin is a digestive tract hormone. It displays pancreatic exocrinogenic, gastrin stimulating, gastric acid secretion inhibiting, insulin insulin pepsin secretion promoting and adipolytic action. It is used as a reagent for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deca:peptide useful as intermediate for secretin - contains histidine, serine, aspartic acid, glycine, threonine, phenylalanine, glutamic acid and leucine
                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                                                                                                                          Porcine; digestive; hormone; pancreatic; duodenal ulcer.
                                                                                                                                       DB 3;
                                                                                                                                     Score 28; DB 3
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Boc-His-Boc
                                                                                                                                                                                                                                                                                                                                                  Intermediate of Secretin synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- Asp-O-t-Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Glu-O-t-Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ser-t-Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= Thr-t-Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= Thr-t-Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Ser-t-Bu
                                                                                                                                                                                                                                                                        P30039 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1; 13pp; Japanese.
                                                                                                                                      50.9%;
55.6%;
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                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
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                                                                                                                                                 Best Local Similarity
Matches 5; Conser
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2 sdgtftsel 10
                                                                                                  10 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                   Seguence
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                  P30039;
                                                                                                                                                                                                                                                 RESULT
P30039
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          Peptides R90945-64 are derived from the factor VIII protein, esp. from a modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to von Willebrand factor, esp. antibodies, thus preventing or treating immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence in P20398 is a precursor for the production of secretin. The peptide sequences given in P20399-402 are peptides which
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                        Strong acid; digestive canal hormone; pancreas; gastrin; pepsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heptacosa:peptide(s) - useful for high yield conversion to high purity secretin on strong acid treatment
                                                                                                                                                             ;
0
                                                                                                                                     Length 10;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konishi
                                                                                                                                     Score 55; DB 17;
Pred. No. 8.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsuchiya Y,
                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Secretin precursor formation peptide 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "OBut protected"
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, Koiwa A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 43; 47pp; English.
                                                                                                                                                                                                                                                                        P20399 standard; Protein; 10 AA
                                                                                                                                     100.0%;
100.0%;
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                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1982-24409E/13
                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                     1 TDGSFTQPLY 10
                                                                                                                                                                                                  AA;
                                                                                                 10
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Modified-site
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                                                                                                                                                                                                                                                                                                                         30-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                      insulin.
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                                                                                                                                                                                                                                                 RESULT
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SSXS

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therapeutically and for immunisation as above.
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                                      Sequence
                                                                                                                                                                                                                                                                                                                                      W92985;
                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                W92985
                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                      SXS
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic peptide having a human leukocyte antigen binding motif #123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response; T cell activation; major histocompatibility complex; cytocoxic T Imphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections. The peptides are therefore useful therapeutically or treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunogenic peptides with HLA binding motif, useful in treatment
study of pancreatic function and as a remedy for duodenal ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Southwood S;
                                                                                                                                              ;
                                                                                                        Length 10;
                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grey HM,
                                                                                                          DB 4;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and diagnosis of cancers and viral diseases
                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celis E,
                                                                                                        Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 31; 150pp; English
                                                                                                                                                                                                                                                                                                                Y45512 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sette A, Kubo RT, Sidney J,
                                                                                                        50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US05039.
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                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1999 (first entry)
                                                                                                                                            5; Conservative
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                                                                                                          Query Match
Best Local Similarity
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2 sdgtftsel 10
                                                    10 AA;
                                                                                                                                                                                 1 TDGSFTQPL 9
                 See also P30038.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                     Y45512;
                                                                                                                                            Matches
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This invention describes the isolation of a novel human muscarinic acetylcholine receptor 6 (mACHR-6), capable of modulating the effects of acetylcholine on acetylcholine responsive cells. mACHR-6 constant of the polypeptides may be used to detect naturally occurring mutations of the mACHR-6 gene and determine if a subject with the mutated gene is at risk of (or is predisposed to have) a mACHR-6 related disorder, modulate cell activity mediated by mACHR-6 (e.g. biological processes mediated by phosphatidylinositol turn-over and signalling), secretion of a molecule, ce.g. a neurotransmitter or a glandular enzymb, or contraction of a molecule, ce.g. a neurotransmitter or a glandular enzymb, or contraction of a molecule, ce.g. a neurotransmitter or a glandular enzymb, or contraction of a molecule, ce.g. nervous system disorders (e.g. amnesia, apraxia, agnosia, amnestic patial disorientation, Kluver-Bucy syndrome, Alzheimer's related memory loss and learning disability, visual, hallucinations, perceptual disturbances, and Levry body dementia with mood swings, and depressive illness), affective disorders, sleep abnormalities, paradoxical sleep abnormalities, paradoxical sleep abnormalities, paradoxical sleep abnormalities, cellorer contracting mechanism disorders (e.g. chornalities during sleep), pain generating mechanism disorders (e.g. characted to irritable bowel syndrome (IBS), or chest pain), movement contraction disorders (e.g. characted to irritable bowel syndrome (IBS), or chest pain), movement
                                                                                                                                                                                         ö
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mACHR-6; muscarinic acetylcholine receptor 6; disorder; secretion; acetylcholine responsive cell; phosphatidylinositol turn-over; smooth muscle cell contraction; nervous system disorder; glandular; schizo-effective disorder; affective disorder; and movement disorder; rat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding muscarinic acetylcholine receptor 6 for modulating the effects of acetylcholine on acetylcholine
                                                                                                             Length 8;
                                                                                                                                                                                         Indels
                                                    Score 27; DB 20; Len
pred. No. 2.1e+05;
                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat mACHR-6 transmembrane domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W92985 standard; Protein; 8 AA.
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                                                                                                             Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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8 AA;
                                                                                                                                                                                                                                                                  4 SFTQPLY 10
                                                                                                                                                                                                                                                                                                                                               2 sfphply 8
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Length 10;

DB 15;

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WPI; 1994-065403/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (CYTE-) CYTEL CORP.
               Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
                                                    4 SFTQPLY 10
                                                                            4 sfphply 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || || || 4 sfphply 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFTQPLY 10
                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-1992;
05-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                 17-FEB-1994.
                                                                                                                                                                                                                                                                                                                        WO9403205-A
                                                                                                                                                                                                                                                                                                 Synthetic.
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                     R49207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
                           Matches
                                                                                                                     RESULT
                                                                                                                              R49207
ID R4
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insulin hypersecretion related obesity), drinking disorders (e.g. diabetic polydipsia), smooth muscle related disorders (e.g. IBS, diverticular disease, urinary incontinence, oesophageal achalasia, and chronic obstructive airways disease), cardiac disorders (e.g pathologic bradycardia or tachycardia, arrhythmia, flutter and fibrillation), and glandular disorders (e.g. xerostomia and diabetes mellitus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is a specific example of a group of new immunogenic peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motific For example, the peptides having an HLA-A3.2 binding motific each have 9-10 residues and contain, from the N-terminus to the C-terminus, (a) a first conserved residue selected from L, M, I, V, S, T, F, C, G, D and E and (b) a second conserved residue of K, R, Y, H or F, where the first and second conserved residue of separated by 6-7 residues. The peptides are capable of binding selected MHC molecules and inducing an immune response. They can be used to treat and/or prevent viral infection and cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also be used to produce antibodies for use as diagnostic or therapeutic agents. The peptides
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                      Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC; major histocompatability complex; viral infection; anticancer; prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide which specifically binds selected MHC allele - used to induce an immune response for treatment or prevention of viral
                                                                                                                               Length 8;
                                                                                                                             Score 27; DB 20; Length 8;
Pred. No. 2.1e+05;
L; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                              Prostate specific antigen-derived HLA-binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection or cancer, or for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can also be used as diagnostic agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 115; 150pp; English.
                                                                                                                                                                                                                                                                    Y38373 standard; Peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kubo RT,
                                                                                                                             49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0027746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      920S-0926666
                                                                                                                                                                                                                                                                                                                      29-SEP-1999 (first entry)
                                                                                                                                                        Conservative
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                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grey HM,
                                                                                                                                                                             3 GSFTQPLY 10
                                                                                         8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA
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1 gafciply 8
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1993;
07-AUG-1992;
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                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                               Y38373;
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                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule; immune response; viral infection; cancer; prostate cancer; lymphoma; hepatitis; AIDS; antibody; diagnosis; prostate specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in R47304-33 and R49201-44 are immunogenic peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif. These peptides may be used in the composition of the invention. These peptides are capable of binding selected MHC molecules and inducing an immune response. They can be used to treat and/or prevent viral infection and cancer, eg. prostate cancer, lymphoma, hepatitis or AIDS. They can also be used to produce antibodies for use as diagnostic or therapeutic agents. The peptides can also be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide which specifically binds selected MHC allele - used to induce an immune response for treatment or prevention of viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                        2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 15;
Pred. No. 27;
Score 27; DB J
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-Al PSA antigen peptide fragment 88-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection or cancer, or for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eaxmple 8; Page 53; 150pp; English
                                                                                                                                                                                                                                                                                          R49207 standard; Protein; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y41894 standard; Peptide; 10 AA.
49.18;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celis E, Grey HM, Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.18; 71.48;
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93US-0027746
                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used as diagnostic agents.
                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y41894;
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Polymerase chain reaction; PCR; primer; amplify; human; T cell receptor; beta chain; TCR; myelin basic protein; BP; autoantigen; encephalitogen; experimental autoimmune encephalomyelitis; EAR; multiple sclerosis; MS; autoimmune disease; neurological disease; cerebrospinal fluid; therapy; central nervous system; complementarity determining region; CDR; T lymphocyte; optical nerve damage; anterior chamber inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R59496-R61666 are immunogenic 10mer peptides that contain a HLM'A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (R71293). R61602 has an IC50 of 0.002 and the sequence occurs at position 1317 in the HBV POL protein. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate
                                                                                                                                                   antigen; epitope; immunogenic target protein; PSA; HBVs; HBVs; HBV; HIVI; plasma specific antigen; hepatiis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; pharmaceutical composition; in vivo; av vivo; threapeutic; pharmaceutical composition; in vivo; av vivo; threapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                           Peptide fragment (1.0796) of HBV binds HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 15,
Pred. No. 1e+02;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 111; 138pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus strain adw.
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57.18;
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93US-0073205.
93US-0159184.
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12-MAY-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-302678/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases.
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Best Local Similarity
Matches 4; Conserv
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4 gtfvspl 10
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                                                                                                                                                                                          Human: rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; BRDI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method has been developed for the diagnosis of human rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                               Rheumatoid arthritis diagnostic protein isoform peptide #45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.3%; Score 26; DB 20; Length 10; 83.3%; Pred. No. 42;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Townsend RR;
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                                       09-DEC-1999 (first entry)
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     electrophoresis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą,
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9947925-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-1999;
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tdasft
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Indels

Sequence

Query Match

R61602

AXXX

RESULT R61602

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Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y55293;
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Y55293
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                                                                                                                                                                                                                                                                                                                                                                                        region 3 (CDR3) of the T cell receptor beta (TCRbeta) chain. These sequences were isolated from cerebrospinal fluid (GSF), spinal cord (SC) and lymph nodes (LN) of clones of Lewis rats with experimental autoimmune encephalomyelitis (BAE). By detecting the presence of a marker TCR vere bias in a body fluid which encapsulates all or part of the target organ, an autoimmune disease (such as a neurological disease) in a human can be identified. This method can also be carried out to detect the presence of a biased motif common to I cell receptors specific for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system can be diagnosed. Therapeutic Vbeta peptide sequences can be selected to use as treatment of a disease or condition. The selection is carried out by identifying a Vbeta gene bias in a body fluid that is not the target tissue or organ of the disease, and selecting an immunogenic peptide corresponding to the Vbeta gene bias. Multiple sclerosis (MS) can be treated by identifying the CDR2 of a V gene peptide on the surface of a T lymphocyte in the CSF of a patient and administering a peptide corresponding to this region. These methods can also be used for the diagnosis and immune-related therapy of optical nerve damage and anterior chamber inflammation as well as other human neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide having a human leukocyte antigen binding motif #2725.
                                                                                                                                                                                                                                                                                                                                                                                R89215-R89251 represent clones of the Vbeta8 complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogenic antigen in a non-target tissue or organ. By analysing the Vbeta gene repertoire of CSF, and determining the presence of a Vbeta gene bias, an immune-related disease that targets the central nervous
                                                                                                                                                                                                                                                                                      Methods for diagnosis and immune-related therapy of autoimmune diseases - partic. multiple sclerosis, by detecting marker T cell receptor V gene bias and treating patients with selected V beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 17; L. Pred. No. 1.6e+02; 0; Mismatches 1;
                                                             /note= "encoded by GGC"
                                                                                                                                                                                                                          Vandenbark AA;
                                                                                                                                                                                               (CONN-) CONNECTIVE THERAPEUTICS INC.
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 6c; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y48114 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.8%;
80.0%;
                                                                                                                                            95WO-US08086
                                                                                                                                                                     94US-0270634
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                       Offner H,
                                                                                                                                                                                                                                                 WPI; 1996-087679/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                  Misc-difference
                                                                                                                                                                                                                                                             N-PSDB; T10618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TOPLY 10
                                                                                                                                                                     01-JUL-1994;
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                                                                                                                                            26-JUN-1995;
                                                                                       WO9601329-A1
                                                                                                                  18-JAN-1996
                                                                                                                                                                                                                       Buenafe A,
                                                                                                                                                                                                                                                                                                                               peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tsply
            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y48114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
δ
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having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are cormally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen fiself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to index a vertical or conditions. They are also useful diagnostically, and can be used to index a vertical or conditions.
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immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCC HB 11885 monoclonal antibody 9079 releasing peptide SEQ 1D NO:187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic peptides with HLA binding motif, useful in treatment diagnosis of cancers and viral diseases \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for influsion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 137; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y55293 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sette A, Kubo RT, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US05039.
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                                                                                                                   vaccine; immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                W09945954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1998;
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97JP-0061727
                                                                                                                                                                   WPI; 2000-136676/12
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Best Local Similarity
Matches 3; Conserv
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Misc-difference 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AA;
                       14-JUN-1994;
                                                                                                                             Al-Abdaly FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 FTQPL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP10243786-A.
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                                                                                                        Guillermo R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||:
2 ytqpi (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W70510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody; non-enzymatic cell selection method; haematopoietic stem cell; haematopoietic progenitor cell; antibody 561; breast cancer cell; antibody 9187; cell surface determinant; diagnostic cell based assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes peptides of 4-17 amino acids which displace either the anti-CD34 monoclonal antibody designated 561, th anti-CD34 monoclonal antibody produced by the hybridoma ATCC HB-11646 (designated 9609), the anti-CD34 antibody produced by hybridoma ATCC HB-11885 (9079), or the anti-human breast cancer antibody produced by hybridoma ATCC HB-11884 (9187), from a cell surface antigen on a target cell. The peptides are useful for displacing antibodies bound to cell surfaces to release cells that have been positively selected by antibody-mediated binding to beads or other solid support. Y55107 to Y5519 represent peptides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Short peptides useful for displacing antibodies from cell surface
                                                                                                                                                                                                                                                                                                                                                     Kobori JA;
Antibody releasing peptide; CD34; hybridoma; binding; antigen; cell surface antigen; identification; haematopoietic stem cell; tumour; cancer; immune system; therapy; displacement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human haematopoietic CD34+ cell binding peptide SEQ ID #187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 20; Length 6; Pred. No. 2.18+05; i Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     Deans RJ, Tseng-Law J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Column 33; 81pp; English.
                                                                                                                                                                                                                                                                                                             NEXE-) NEXELL THERAPEUTICS INC.
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                                                                                                                                                                                                                            95US-0482228
                                                                                                                                                                                                                                                                                                                                                     Helgerson SL,
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                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-590399/50
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Best Local Similarity
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2 ytqpi 6
                                                                                                                                                                                                                                                                                                                                                 Guillermo R,
Al-Abdaly FA;
                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 FTQPL 9
                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                     14-JUN-1994;
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                                                                                                                                          JS5968753-A
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                                                                                                                                                                                    19-OCT-1999
                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigens.
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peptide, and was used to test the method of the invantion. The method is a non-enzymatic method for the positive selection of one or more target cells from a heterogeneous cell suspension, by using specific peptides which effect the displacement and release of a specific target cell from a specific monoclonal antibody. The method is useful for positive selection and specific release of target human haematopoletic stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and the antibody 561. The method is also useful from a patient's blood or specific release of target human breast cancer cells, bound by the conoclonal anti-Drasst cancer antibody 9187, from a patient's blood or bone marrow. Identification of peptide epitopes for antibodies which recognise cell surface determinants also allows construction of diagnostic cell based assays. The peptide mediated release is enzyme from and thus leaves the cell surface profeins inteat moreover, peptide mediated release laaves the target cell free of bound antibody or antibody fragments. The method also produces a high yield of functional carry cells and is relatively inexpensive to carry out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                              Non-enzymatic method for the positive selection of target cells from a heterogeneous cell suspension, useful for selecting human breast cancer cells from a patient's blood or bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a human haematopoietic CD34+ cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli glucose dehydrogenase; GDH; PQQ; PQQDH; glucose;
pyrrologuinoline guinone coenzyme.
                                                                                                                                                                Koborl JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Changed from His in wild-type to Asp in mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                Tseng-Law J,
                                                                                                                                                            Deans RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 9; Column 38; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                (NEXE-) NEXELL THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W70510 standard; peptide; 7 AA.
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94US-0259427
                                                                                                                                                                Helgerson SL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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The invention relates to a synthetic multivalent complex for binding to a major histocompatibility complex (MHC)-peptide complex. The multivalent complex comprises a T-cell receptor (TCR) protein, preferably fused to a leucine zipper sequence from c-jun or c-fos for stabilising the TCR complex. Sequences Y56066-Y56075 represent the N-termini of alpha and beta dail genes from a range of HLA restricted TCR proteins. This sequence represents the N-terminus of the human Vbetal7 chain from an influenza matrix peptide HLA-A0201 restricted TCR, encoded by clone JM22. The multivalent TCR complexes are useful for detecting MHC-peptide complexes and delivery of therapeutic agents to target cells, in vivo. The specificity of the TCRs enables the localization of the Inposome-contained drugs to the desired target site such as a tumour or virus-infected cell. This would be useful in many situations and in patigues and therefore are not all detected by the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 22; DB 21; Length 9; 66.7%; Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 17, 2001, 13:39:47 Job time: 157 sec
                   Example 10; Fig 20B; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; T-cell receptor; c-jun; leucine zipper motif; tumour; influenza virus matrix protein epitope; major histocompatibility complex; immune system; PCR primer; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                  enzymes are claimed to allow highly sensitive and selective quantitative determination of glucose.
                                                                                                                                                                                                                         The present sequence represents a modified region (residues 772-778) of the Escherichia coli glucose dehydrogenase (GDH) comprising of a single residue mutation H7550, i.e. where residue 4 (representing residue 775 of GDH) is changed from H1s to Asp. The invention provides modified E. coli GDH enzymes, which are modified at residue 775, with their pyroloquinoline quinone (PQC) coenzyme. A GDH enzyme with its PQC coenzyme is known as PQCPH. The invention also provides the gene encoding the modified PQCDH enzyme. The modified PQCDH coenzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence was not provided by the inventors but was made up using the wild-type region, representing residues 772-778 of GDH, and other relevant information provided in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                Modified glucose dehydrogenase - allows sensitive and selective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminus of human Vbetal7 chain HLA-A0201 restricted TCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 22; DB 19; Length 7; 100.0%; Pred. No. 2.1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                      quantitative determination of glucose
                                                                                                                                                                                        Disclosure; Page -; 5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y56067 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2000 (first entry) -
               97JP-0061727
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N-PSDB; 247257.
                                                                                           WPI; 1998-549782/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 4; Conserv
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                                                     (HAYA/) HAYADE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA;
               03-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9960119-A2
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4 dqsf 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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δλ
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Gaps .; 0

2; Indels

0; Mismatches

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:38:41 ; Search time 13.63 Seconds (without alignments) 49.817 Million cell updates/sec Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-765-837-3 55 1 TDGSFTQPLY 10 Title: Perfect score: Sequence: Scoring table:

195891 seqs, 67900655 residues Searched:

1097 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	carnocin UI49 - Ca	polygalacturonase	T-cell receptor be	Ig heavy chain DJ	bHLH transcription	leucopyrokinin - M	macrophage chemota	3-oxoacid CoA-tran	lectin GNL2 alpha	Ig heavy chain CRD	e]]	Ig mu chain D regi	lin	ribosomal protein	alpha-2-macroglobu	hypothetical prote		variant surface gl	Ig heavy chain CRD	T-cell receptor be	lectin - potato (f	phosphoenolpyruvat	[Phe-6]-mosact - s	T-cell receptor qa	triacylglycerol li	variant surface ql	vitellogenin, 190k	Ig heavy chain CRD	anglotensin precur
	B ID	A5	2 C61440	2 PH0948									2 E33932												_		2 E61512	2 A61622	2 PT0243	2 A90345
	Length DB	7	10	10	10	9	80	σ	6	10	10	S	7	8	6	10	10	10	9	9	7	80	6	σ	6	10	10	10	10	10
د د د	Match	32.7	32.7	C3	30.9	29.1	29.1	29.1	29.1	29.1	ď.	ζ.	۲.	٠	۲.	ζ.	27.3	ζ.	'n	'n	25.5	Ġ	'n	ı.	'n.	'n	'n.	'n	'n.	'n.
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+[1000	Nesut L		7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Caps

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Query Match
32.7%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels

|:|| 3 GAFT 6 3 GSFT 6

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T-cell receptor be	phagocytosis-stimu	Ig heavy chain CRD	T-cell receptor be	T-cell receptor be	T-cell receptor be	T-cell receptor be	neuropeptide GNFFR	large granule 1.3 c	T-cell receptum be	T-cell receptor be	neural cell adhesi	virotoxin - destro	peptidyl-dipeptida	leghemoglobin III	urine glycopeptide
PH0925	A02147	PT0271	PT0699	PT0657	PT0720	PT0589	A43129	PC1316	PT0523	PT0689	A39690	A58725	A32523	S20162	хсниеи
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14 25	13	13	13	13	13	13	13	13	Η	13	13	13	13	13	13

ALIGNMENTS

Gaps

0;

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macrophage chemotactic factor - human (fragment)
N.Alternate names: T-cell hybridoma D6-18 protein
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 23-Feb-1997
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 23-Feb-1997
C;Accession: A37027
R;Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
Cell. Immunol. 123, 212-225, 1989
A;Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clo
A;Reference number: A37027; MUID:89376581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A22967
R;Nachman, R.J.; Holman, G.M.; Cook, B.J.
Biochem. Biophys. Res. Commun. 137, 936-942, 1986
A;Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: stru A;Reference number: A23967; MUID:86269041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leucopyrokinin - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 11-Jul-1997
                   A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-6 <2HA>
A;Cross-references: GB:S79038; NID:g1042006; PIDN:AAD14294.1; PID:g4261994
C;Genetics:
A;Gene: XIdIb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-8 <NAC>
C; Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 8/Modified site: amidated carboxyl end (Leu) #status experimental
                                                                                                                                                                                                                                           Length 6;
                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 2; Length 8; Pred. No. 2e+05; 2; Indels
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                                                                                                                                                                                                                                        Score 16; DB 2;
Pred. No. 2e+05;
1; Mismatches
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66.7%;
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Best Local Similarity
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A;Molecule type: protein
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 4; Conserv
A; Accession: 151317
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1 SATEP 5
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                                         T-cell receptor beta chain V-D-J region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 19-Oct-1995 #text_change 30-May-1997
C;Accession: PH0948; PH0897; PH0909; PH0899
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerging A;Reference number: PH0891; MUID:92078857
A;Accession: PH0891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain DJ region (clone C100-91A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1344
S:Wasserman, R.; Gallii, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761
                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-10 <GO1>
AExperimental source: myelin basic protein fragment-reactive T-cell, recovered from exp
A;Accession: PH0897
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: myelin basic protein-immunized T-cell, clones 3, 6-2, 14, hybridd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 2.2e+03;
2; Mismatches 2; Indels
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ches 2;
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Pred. No. 1.4e+03
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-10 <WAS>
C;Keywords: heterotetramer; immunoglobulin
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42.9%;
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A;Residues: 1-10 <GO4>
A;Experimental source: clone 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.7
Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-10 <GO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-10 <GO3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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2 SDGDWGQ 8
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R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated qur. A;Reference number: A33932; MUID:89282823
A;Accession: E33932
                                                                                                                                                                                                                                   cell receptor beta chains have few N regions
                                                                               T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1,)
C;Accession: PT0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig mu chain D region (E7) - mouse
C;Species: Was musculus (house mouse)
C;Date: 09-Mar.1990 #sequence_revision 09-Mar-1990 #text_chauge 16-Aug-1996
C;Accession: E33932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Aspergillus ficuum
C;Species: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: PT0030
R; Ettalibi, M.; Baratti, J.C.
Agric. Biol. Chem. 54, 61-68, 1990
A; Title: Molecular and kinetic properties of Aspergillus ficuum inulinascs.
A; Reference number: PT0030; MUID:90344234
A; Accession: PT0030
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A;Residues: 1-8 <ETT>
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15; DB 2;
Pred. No. 2e+05;
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                                                                                                                                                                                                         J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T A;Reference number: PT0509; MUID:91277601
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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A;Molecule type: mRNA
A;Residues: 1-7 - CBAC>
A;Cross-references: GB:M271
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: inulase
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Best Local Similarity
Matches 3; Conserv
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C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: Pr309
R; Yamada, M:; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: PT0222; MUID:91108337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lectin GNL2 alpha chain - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: 383806
R;Kamemura, K.; Furuichi, Y.; Umekawa, H.; Takahashi, T.
Biochim. Biophys. Acta 1158, 181-188, 1993
A;Title: Purification and characterization of novel lectins from Great Northern bean, A;Reference number: 538304; MUID:94002183
A;Status: preliminary
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                     C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
                                                            C; Accession: PD0443
R; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID. August 1998
A; Description: Proteome analysis of mouse brain.
A; Reference number: PD0441
A; Contents: Striatum
A; Moccasion: pD0443
A; Molecule type: protein
A; Residues: 1-9 < KAW>
C; Keywords: CoA-transferase
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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3-oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 2; I
Pred. No. 3.4e+03;
2; Mismatches 4;
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2e+05;
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Pred. No. 3.4e-
2; Mismatches
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Pred. No.
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A; Molecule type: DNA
A; Residues: 1-10 (YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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33.3%;
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40.0%;
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50.0%;
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Best Local Similarity 40.0
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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2 TETSFS 7
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4 YTDPV 8
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C;Species: Mycobacterium boyis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C;Caccesion: 33698
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac A;Accession: S36898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: S33844
C;Accession: S33844
Eur. J. Biochem. 214, 803-809, 1993
A;Title: Hydrocortisone induces the synthesis of alpha(2)-macroglobulin by rat mammary A;Reference number: S33843; MUID:93307297
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A.Residues: 1-10 <WAR>
C.Superfamily: alpha-2-macroglobulin
C.Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester bond
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44.4%; Pred. No. 5.3e+03;
***cmatches 2; Indels
  Score 15; DB 2; Length 8; Pred. No. 2e+05; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+05;
Matches 2; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                ribosomal protein S8 - Mycobacterium bovis (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 < CHA>
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-2-macroglobulin - bovine (fragment)
    27.3%;
Query Match
Best Local Similarity 40.0°
Matches 2; Conservative
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Best Local Similarity 44.4
Matches 4; Conservative
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Search completed: January 17, 2001, 13:40:19 Job time: 98 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

January 17, 2001, 13:39:51; Search time 8.5 Seconds (without alignments) 37.993 Million cell updates/sec Run on:

US-08-765-837-3 55 1 TDGSFTQPLY 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 seqs, 32294092 residues Searched:

329 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	Description	P22396	010581	P36960	P82157	P23210	P21143	P13049	P40686	P19853	P30089	P01017	P01858	P41966	P42984	P02729	P81731	P41488	P81545	P13736	P13737	P25418	P14595	P41872	P41486	P04549	P19989	P15507	P81813	P38556	P80975	P43172	P41868	P19344
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)ta;	T.K., Nachman R.J., de Loof A.; synthesis of locustamyotrupin II, ista migratoria. Member of the ("",") MUSCLE CONTRACTILE ACTIVITY PYROKININ FAMILY.	ė		2081 ⁷	Picarelli 2.P
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PRT; 8 AA ed) sequence update)	annotation update) 2). ry locust). odd: Tracheata: He teroidea: Orthopte crididae: Locusta.	Hayes T.K., Nachman nn and Synthesis of 15 Locusta migratoris family."; 14(1990). SCERAL MUSCLE CONTRA	; 1. rokinin. 26341771A9CAA87B CRC64 Score 20; DB 1; Le Score 20; DB 1; Le 1. Mismatches 3.		D; PRT; 10 AA. Created) Last sequence update) Last annotation update) DE I (FRAGMENT): ordata; Craniata; Verte i Scleroglossa; Serpent Bothrops.	Carm
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PRT;	annotatio 2). .ory locust .poda; Trac .pteroidea;	Hayes T.K in and syn if Locusta family."; 4(1990). SCERAL MU	1. Okinj AMII 63417 SCOI Prec		PRT; 1) equencent anotat FRAGME; Cran roglos	agor.
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(Re	LANG-1991 (Rel. 19, Last annotation update) LOCUSTANYOTROPIN 2 (LOM +NT-2). LOCUSTA migratoria (Migratory locust). LOCUSTA migratoria (Migratory locust). EDKATYOTE: Metazoa; Arthropoda; Tracheate; Hexapoda; Insect Pterygotea; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acrididae; Locusta.	SEQUENCE. TISSUE-CORPORA CARDIACA; Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof "Isolation identification and synthesis of locustamyotropic additional neuropeptide of Locusta migratoria. Member of th cephalomyotropic peptide family."; Insect Biochem. 20:479-484(1990)	PROSITE: PS00539; PYROKININ; 1. WOULOPEPLIDE: Amidation; Pyrokinin. WOLERES SEQUENCE 8 AA; 934 MW; 26341771 TY Match 36.48; SCOTE TY Local Similarity 50.08; Pred.	21. 9 - 31. 8	BOTJA BOTJA ANGL_BOTJA STANDARD; PRT; 10 AA. Q10581; 01 AA. Q10581; 02 A. Created) Q10-CCT-1996 (Rel. 34, Last sequence update) Q10-CCT-1996 (Rel. 37, Last annotation update) MOLOCT-1998 (Rel. 37, Last annotation update) ANGLOPENSIN-LIKE PEPTIDE I (FRAGMENT): Bothrops jararaca (Jararaca). Ebtaryota: Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colviperidae; Crotalinae; Bothrops. SEQUENCE.	MEDLINE=96208932; Pubmed=8829801; Borgheresi R.A.M.B., Dalle Lucca
LT 1 LOCMI LMT2_LOCMI P22396; 01-AUG-1991 01-AUG-1991	MYOTH MYOTH Ta; Pta; Pta; Pta; Pta; Pta; Pta; Pta; Pt	E. L., lion, myoti myoti myoti myoti myoti myoti ILAR	ptide ptide E E	DGSFTQPL :1 1 EGDFTPRL	1996 11996 11998 11998 NSIN S jan S jan Eta; R	esi l
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-!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
ACTIVE ON GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92321768; PubMed-1622206;
Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification and characterization of a new bacteriocin isolated from
                                                                                                                                                        Gaps
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Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Tortricoldea; Tortricidae; Olethreutinae; Cydia.
"Isolation and identification of angiotensin-like peptides from the
                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 31, Last annotation update)
LANTIBIOTIC CARNOTIN U149 (FRAGMENT).
Carnobacterium Sp. (strain U149).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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'Davey M., East P.D., Thorpe A.;
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1; Mismatches 5;
                                                                                                                              Score 19; DB 1;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYDIASTATIN 6.
           plasma of the snake Bothrops jararaća.";
Comp. Biochem. Physiol. 113B:467-473(1996).
-!- SIMILARTY: BELONGS TO THE SERPIN FAMILY.
INTERPRO: IPR000215; -.
PROSITE; PS00284; SERPIN; PARTIAL.
VASOCONSTRICCT: Plasma; Serpin.
                                                                                                                                                                                                                                                              7 AA.
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MEDLINE=98054539; Pubmed=9392829;
                                                                                                                              Query Match 34.5%;
Best Local Similarity 33.3%;
Matches 3; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FONGTION: COMPONENT OF THE BASAL LAXER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.
-!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
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01-NOV-1991 (Rel. 20, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
CAPSID ASSEMBLY AND DAM MATURATION PROTEIN (VIRION PROTEIN UL38)
(CAPSID PROTEIN VP19C) (FRAGMENT).
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"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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MEDLINE=91101287; PubMed=1846198;
Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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8 AA; 936 MW; 0B2879C45B573767 CRC64;
                                                                                                                                                                                                                          32.7%; Score 18; DB 1; L 100.0%; Pred. No. 8.9e+04; Live 0; Mismatches 0;
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
LEUCOXININ IV (L-IV).
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                                                                                      Neuropeptide; Amidation.
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SEQUENCE 8 AA; 936 MW;
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                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MYOTROPIC ACTIVITY).
-!- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
                                                                                                                       Cephalomyotropins.";
Comp. Biochem. Physiol. 84C:271-276(1986).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILLE
--- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                  Holman G.M., Cook B.J., Nachman R.J.;
"Primary structure and synthesis of two additional neuropeptides
from Leucophaea maderae: members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87052651; PubMed=2877794;
Holman G.M., Cook B.J., Nachman R.J.;
Primary structure and synthesis of a blocked myotropic
"Primary structure and synthesis of a blocked myotropic
neuropeptide isolated from the cockroach, Leucophaea maderae.";
Comp. Biochem. Physiol. 85C:219-224(1986).
-I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Trachéata, Hexapoda, Insecta,
Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria,
Blaberoidea, Blaberidae, Leucophaea.
           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                Score 16; DB 1; Length 8;
Pred. No. 8.9e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nachman R.J., Holman G.M., Cook B.J.; Active fragments and analogs of the insect neuropeptide
                                                                                                                                                                                                              8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   949 MW; 92341771A9D5A1B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leucopyrokinin: structure-function studies.";
Biochem. Biophys. Res. Commun. 137:936-942(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
LEUKOPYROKININ (LEW) (LEM-PK).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                       8 AA.
                                                                                                                                                                                                    AMIDATION.
 Leucophaea maderae (Madeira cockroach)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION
                        Pterygota; Neoptera; Orthopteroidea.
Blaberoidea; Blaberidae; Leucophaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide; Amidation; Pyrokinin.
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-86269041; PubMed-3015140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00539; PYROKININ; 1.
                                                                                                                                                                                                                                                  Match 29.1%;
Local Similarity 75.0%;
les 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                      Neuropeptide; Amidation.
                                                            SEQUENCE, AND SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A23967; A23967.
INTERPRO; IPR001484;
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                                                                         TISSUE-HEAD
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P13049;
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Best Local Si
Matches
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MOD_RES
SEQUENCE
                                                                                                                                                                                                               SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-! FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-! CATALYTIC ACTUTIY: APP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.
-! SUBDINIT: MONOMER (BY SIMILARITY).
-! MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYGOSYL OXIGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME SA DAMA STRAND.
-! SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gap.,
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                         P40686;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
DNA TOPOLSOWERASE I (EC. 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
(UNTWISTING ENZYME) (SWIVELASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87194810; PubMed-3032952; Ostrowski J., Jagura-Burdzy G., Kredich N.M.; Ostrowski J., Gagura-Burdzy G., Kredich N.M.; Sequences of the cysB regions of Salmonella typhimurium and Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Score 16; DB 1; Length 8;
Pred. No. 8.9e+04;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA; 1145 MW; 2C25B67B02D37338 CRC64;
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PROSITE; PS00396; TOPOISOMERASE_I_PROK; PARTIAL.
ISOMerase; Topoisomerase; DNA-binding.
NON_TER
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P19853;
01-FEB-1991 (Rel. 17, Created)
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29.1%;
66.7%;
                                                                 4; Conservative
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Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Elliott D.F., Peart W.S.,
"The amino acid sequence in a hypertensin.";
Blochem. J. 65:246-254(1957).
-: FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
     ANGIOTENSINOGEN [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II] (FRAGMENT)
                                                                                                                                                                                                    CLEAVES ANGIOTERNSIN I, FROM ANGIOTERSINGEN. ACE (ANGIOTERSIN ENLIRE PRESSORES ANGIOTERNSIN I, FROM ANGIOTERSINGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KOMMON, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.
                                                                                                                                                                                                                                                                                             -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
PIR; A01250; A01250.
PIR; A90345; A90345.
INTERPRO; IPRO00215; -.
                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom i;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoiuea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14; DB 1; Length 10; Pred. No. 3.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEEFBDD761F2DB42 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                  4 AA
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21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
PHAGOCYTOSIS-STIMULATING PEPTIDE (TUFTSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO00215; -.
PROSITE; PS00284; SERPIN; PARTIAL.
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22.2%;
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1282 MW;
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                                                                                        Bovidae; Bovinae; Bos.
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nes 2; Conserv
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1 DRVYVHPFH 9
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P01858;
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SEQUENCE
                                                                                                                          SEQUENCE
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                                                                                                                                                                                                    "Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin Clypeaster japonicus."; Zool. Sci. 4:649-656(1987).
-!- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
PIR; JN0027; JN0027; JN0027.
SEQUENCE 9 AA; 924 MW; 93245729CDC5BAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
Electrophoresis ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.6, ITS MW IS: 46 KDA.
SWISS-2DPAGE; P30089; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 11) (FRAGMENT).
                                                 Clypeaster japonicus (Sand dollar).
Sukaryota: Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroida;
Clypeasteridae; Clypeaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                      TISSUE=EGG JELLY;
Suzuki N., Kurita M., Yoshino K.I., Kajiura H., Nomura K.,
                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Pred. No. 8.9e+04;
...matches 0;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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Last annotation update)
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(Rel. 40, Last anno
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40.0%;
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Best Local Similarity
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Matches 2; Conserv
                                 PHE-6]-MOSACT.
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                                                                                                                                                                                           Yamaguchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                1 TDGSF 5
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21-JUL-1986 (
01-OCT-2000 (
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2 PLF 4
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P01017;
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SEQUENCE
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UPA3_HUMAN

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ANGT_BOVIN RESULT

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Search completed: January 17, 2001, 13:41:34 Job time: 103 sec
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GLUR_HUMAN
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"GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
the sheep tapeworm, Moniezia expansa."; 1060(1993).
Blochem. Blophys. Res. Commun. 193:1054-1060(1993).
-: SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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-:- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
                                                                                                                                                                                                                                                                                                                                                                                              Moniezia expansa (Sheep tapeworm).
Eukaryota; Metazoa; Platyhelminthes; Neodermata; Cestoda; Eucestoda;
Cyclophyllidea; Anoplocephalidae; Moniezia.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-1995 (Rel. 32, Last sequence update)
12-NOV-1995 (Rel. 32, Last sequence update)
12-NOV-1995 (Rel. 32, Last sequence update)
12-NOV-1995 (Rel. 32, NoV-1996)
13-NOV-1995 (Rel. 32, Rel. 
Score 13; DB 1; Length 4;
Pred. No. 8.9e+04;
0; Indels
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6 AA; 787 MW; 69D409C9C4481000 CRC64;
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6DD73768745B5DB0 CRC64;
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TISSUE-HEAD;
MEDLINE-95380343; PubMed-7651886;
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             23.6%;
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PIR; A03188; XGHUEU.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDITARE 72062338; PubMed-5126885;
Lote C.J., Weiss J.B.;
"Identification in urine of a low-molecular-weight highly polar
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Score 13; DB 1; Lengtn /,
Pred. No. 8.9e+04;
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8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycopeptide containing cysteinyl-galactose."; Biochem. J. 123:25P-25P(1971).
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21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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ilarity 33.3%;
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Best Local Similarity 66.73
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Best Local Similarity
Matches 2; Conserv
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CARBOHYD
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P02729;
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                              January 17, 2001, 13:39:31
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Listing first 45 summaries

    protein search, using sw model

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ALIGNMENTS

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Laurencia
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;
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                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                           Lewis S.M., Valdes F., Frias I., Hernandez-Gonzalez M.C., Lewis S.M., Valdes F., Frias I., Hernandez-Gonzalez M.C., Gacesa P.; "Analysis of rDNA and RUBISCO spacer sequences of the genera and Osmundea in the Canary Islands."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 3.7e+05;
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PRELIMINARY;
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Davis T.R., Tabatebal L., Bruns K., Hamilton R.T., Nilsen-Hamilton M.; "Basic fibroblast growth factor induces 3T3 fibroblasts to synthesize and secrete.a cyclophilin-like protein and beta 2-microglobulin."; Biochim. Biochim. Biochim. 943, 963 MW; D6D27731A9D6D87D CRC64;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBL_TaxID=10095;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
SUPERINDUCIBLE PROTEIN 24, SIP24-CYCLOPHILIN HOMOLOG, PEAK C.
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MEDLINE-20022990; PubMed-10555290;
Clark M.A., Moran N.A., Baumann P.;
"Sequence evolution in bacterial endosymbionts having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=9;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
NIFS PROTEIN HOMOLOG (FRAGMENT).
        995BDDDDC4140AB1 CRC64;
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Pred. No. 3.7e+05;
                                                                             Score 18; DB 2;
Pred. No. 3.7e+05;
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EMBL; AF130812; AAF13797.1; -.
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Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                32.7%;
50.0%;
     9 AA; 1027 MW;
                                                                                                                                     4; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
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SEQUENCE
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papillionoideae; Glycine.
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
PROPEINASE 3 (FRAGMENT).
Mus musculus (Mouse).
Mus musculus (Mouse).
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musiculus; Mouse).
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1904;
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Pred. No. 1.8e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SV129 D3;
Lutz P.G., Moog-Lutz C., Houzel-Charavel A., Cayre Y.E.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ007030; CAA07429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 11; Length 9;
Pred. No. 3.7e+05;
1; Mismatches 2; Indels
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Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
EMBL; M33704; AAA26724.1; -.
NON_TER
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Last annotation update)
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Phytochemistry 31:731-735(1992).
SEQUENCE 10 AA; 975 MW; 3C733271A879D1B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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50.0%;
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ilarity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.5
Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity
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2 DPTFGTPL 9
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3 GSYPSP
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SEQUENCE
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RESULT 098905

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Q9RQ49 Q9RQ49;

RESULT 09R049

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MEDLINE-95102521; pubMed-7804141;
Takahashi M., Moriguchi S., Yoshikawa M., Sasakl R.;
Moriguchi S., Yoshikawa M., Sasakl R.;
Isolation and characterization of oryzatensin: a novel bloactive peptide with ileum-contracting and immunomodulating activities derivad from rice albumin.";
Biochem. Mol. Biol. int. 33:1151-1158(1994).
SEQUENCE 9 AA: 1093 MW; 0E8C67377B56877B CRC64;
                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-SKIN SECRETION;
washitz F.A., Bowle J.H., Tyler M.J., Wallace J.C.;
Peptides from the skin glands of the Australian buzzing tree froy Litori electrica. Comparison with the skin peptides from Lito.i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rubella.";
Aust. J. Chem. 52:0-0(1999).
-!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
-INTIBIOTIC ACTIVITY.
-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
Amphibian skin.
sEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5;
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Pred. No. 3.7e+05;
1; Mismatches 0; Indels
                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
0RYZATENSIN-BIOACTIVE PEPTIDE.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 3.2.
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                PRT;
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29.1%;
Best Local Similarity 66.7%;
Matches 2; Conservative 1
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Best Local Similarity 75.0
Matches 3; Conservative
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                PRELIMINARY;
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3 PMY 5
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P82073
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P82099
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Clark M.A., Moran N.A., Baumann P.;
"Sequence evolution in bacterial endosymbionts having extreme base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-96175156 pubMed-9110934;

Svensson A.C., Setterblad N., Pihlgren U., Rask L., Andersson G.;

"Evolutionary relationship between human major histocompatibility
complex HiA-DR haplotypes.";

Immunogenetics 43:304-41(1996).

EMBL; X88792; CAA61271.1;
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                                                                                                                                                                                                                                  Proteobacteria; gamma subdivision; Buchnera
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, Last annotation update)
                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
NIFS PROTEIN HOMOLOG (FRAGMENT).
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Pred. No. 3.7e+05;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                              compositions.";
Mol. Biol. Evol. 16:1586-1598(1999)
EMBL; AF130814; AAF13805.1; -.
                                                                                        PRT;
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Best Local Similarity 66.7%;
Matches 2; Conservative
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8 AA; 909 MW;
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                                                                                      PRELIMINARY;
                                                                                                                                                                                                                   Buchnera aphidicola
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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4 PIY 6
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REPLINE-20196006; PubMed=10731132;

REDLINE-20196006; PubMed=10731132;

RADLINE-20196006; PubMed=1078.

RADLINE-20196006; PubMed=1078.

RADLINE-20196006; RADLINE-20196; RADLINE-20196;
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     MEDLINE=92129337; PubMed=1733949;
Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cloce V.,
Schiffmann E., Liotta L.A.;
                                                                                                                                                                                                                                                                                             "Identification, purification, and partial sequence analysis of autotexin, a novel motility-stimulating protein."; J. Biol. Chem. 267:2524-2529(1992). SEQUENCE 10 AA: 1171 MW: 736F44577AFIB2CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB 4; Length 10;
Pred. No. 1.1e+04;
       Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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CG18256.
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Matches 3; Conservative
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                                                                                                                                                    NCBI_TaxID=9606;
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                                                      AUTOTAXIN.
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MEDLINE-96355846; PubMed-8751884;
Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "cis Elements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                             Wabbitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
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Pred. No. 3.7e+05;
1; Mismatches 2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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Pred. No. 3.7e+05;
1; Mismatches 0;
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                                                                          Litoria rubella (Desert tree frog).
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Infect. Immun. 64:3451-3460(1996).
EMBL; U51862; AAB88721.1; -.
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40.0%;
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Amphibian skin; Amidation.
MOD_RES 5 5
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                                                                                                                                                                      NCBI_TaxID=104895;
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                                                                                                                                                                                                                                                                                                                                       rubella.";
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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong Y.H., Zhong F.N., Zhong W., Zhu S., Zhu S., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Science 287:2185-2195(2000).

EMBL, AE003488; ARHABI31; ...
FLYBASE: FBGn003380; CG18256.
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SEQUENCE FROM N.A.

Brouillette J.A., Andrew J.R., Venta P.J.;

Brouillette J.A., Andrew J.R., Venta P.J.;

Brouillette J.A., Andrew J.R., Venta P.J.;

"Estimate of Nucleotide Diversity in Dogs Using a Pool-and-Sequence Method to Identify Single Nucleotide Polymorphisms.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF202073; AAF20918.1; -.

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SEQUENCE 8 AA; 899 MW; 6731A1E059CAA867 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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THYMIDYLATE SYNTHASE (FRAGMENT).
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SEQUENCE 7 AA; 817 MW; 69C737644731A740 CRC64;
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Matches 3; Conservative
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OM protein - protein search, using sw model

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Perfect score: 55
Sequence: 1 TDGSFTQPLY 10

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 52832

174772 seqs, 17957048 residues

Searched:

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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 1226, Appl Sequence 109, Appl Sequence 109, Appl Sequence 1187, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 108, Appl Sequence 108, Appl Sequence 8, Appl Sequence 8, Appli 9, Appli 8, Appli 8, Appli 100, APP 5208144 5208144 Appl Appl Appli Appl Appl Sequence 14, Appl 14, App] Sequence 100, Patent No. 5208 Patent No. 5208 Sequence 1, Sequence 46, Sequence 1: Sequence 1: Sequence 1: Sequence 6: Sequence 1: Sequence 1: Description Sequence 3 Sequence US-09-165-543-34 US-08-159-339A-109 US-08-482-228-187 US-08-190-788A-64 US-08-3474B-69 US-08-465-391A-64 US-08-465-391A-64 US-08-464-538B-64 US-08-464-538B-64 US-08-464-538B-64 US-08-482-228-8 US-08-482-528-8 US-08-482-528-8 US-09-173-941-100 5208144-38 US-09-173-941-100 S208144-38 US-08-470-702-14 US-08-470-702-14 US-08-470-702-14 US-08-470-702-14 US-08-467-831-14 US-08-467-831-14 US-08-467-831-14 US-08-467-831-14 US-08-985-090-14 US-08-159-339A-1226 US-08-789-588-15 US-08-486-0578-17 US-08-541-033A-6 US-08-789-588-17 US-08-602-725-8 Query Match Length Score Result Š

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Sequence 18: App Sequence 18: App Sequence 28, App Sequence 28, Appl Sequence 28, Appl Sequence 20, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 8, Appl Sequence 8, Appl Sequence 8, Appl	Patent No. 5210075 Sequence 1, Appli Sequence 136, App Sequence 138, App
US-08-828-451-6 US-08-482-228-185 US-08-482-228-185 US-08-482-228-185 US-08-482-228-28 US-08-482-228-28 US-08-863-813A-20 5514646-17 US-08-297-731-7 US-08-297-731-8 PCT-US95-10793-8	5210075-47 102-07-865-216B-1 US-08-482-228-136 US-08-482-228-138
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RESULT.

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Sequence 14, Application US/08985090

Patent No. 58850

Sequence 13, Application US/08985090

Sequence 14, Application US/08985090

Sequence 14, Application US/08985090

SERVET SEQUENCES: 28

CORRESPONDENCE ADDRESS: 28

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CORPUTER READABLE FORM:

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COMPUTER: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/985,090

FILING DATE:

PROFERENT INFORMATION:

NAME: Javentin RECENT INFORMATION:

NAME: Javentin RECENT INFORMATION:

TELEPHONE (61/71/227-740)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 109, Application US/08159339A

Sequence 109, Application US/08159339A

Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Cette, Alessandro
APPLICANT: Cette, Alessandro
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-MG-1992
APPLICATION NUMBER: US 08/027,746
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)742-4214
INFOMMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-165-543-34
        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GSFTQPLY 10
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                                                                                                                                                                                                                          FILING DATE:
                                                   02109
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                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: ANDERVE D. 3. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8;
                                                                                    APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 3; Le
Pred. No. 1.3e+05;
0; Mismatches 2;
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                          COUNTY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           018623-005030US
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US-08-159-339A-1226
; Sequence 1226, Application US/08159339A
; Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 49.1%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-159-339A-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                     GENERAL INFORMATION:
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US-09-165-543-34
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                           CITY: STATE:
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APPLICANT: Kobori, Joan A.
APPLICANT: Kobori, Joan A.
APPLICANT: A1-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgerson, Sam L.
APPLICANT: Helgerson, Sam L.
APPLICANT: Beans, Robert J.
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 3; Length 6;
Pred. No. 1.3e+05;
2; Mismatches 0; Indels
                                                                                                          0; Indels
                                                                      Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: O7-JUN-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: 35,170
RECISTRATION NUMBER: 35,170
TELEPHONE: (714) 440-5353
TELEPHONE: (714) 540-5353
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHRACTERISTICS:
LENGTH: 6 Anino acids
                                                                 Score 22; DB 2; 1
Pred. No. 1.3e+05;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: Janice Guthrie, Ph.D. STREET: P.O. Box 15210 CITY: Irvine STATE: California COUNTRY: USA ZIP: 97113-5210 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N. Sequence 64, Application US/08190788A Sequence 64, Application US/08190788A Patent No. 5608035 SEGURAL INFORMATION: APPLICANT: Yanofsky, Stephen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       US-08-482-528-187; Sequence 187, Application US/08482528; Patent No. 6017719; CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.08;
                                                                    40.08;
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                 Query Match 40.0
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-482-528-187
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2 YTOPI 6
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2 YTQPI 6
      US-08-482-228-187
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Patent No. 5968753

GENERAL INFORMATION:

APPLICANT: Tseng-law, Janet
APPLICANT: Tseng-law, Janet
APPLICANT: Al-Andaly, Fahad A.

APPLICANT: Guillermo, Roy
APPLICANT: Helgerson, Sam L.

APPLICANT: Deans, Robert J.

TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 3; Length 10;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-010-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: 35,170
TELECOMMUNICATION INFORMATION:
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-MG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REERENEE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELLERAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Janice Guthrie, Ph.D. P.O. Box 15210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (714) 440-5533
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                 109:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA ZIP: 92713-5210 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Irvine
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SFTQPLY 10
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STREET: P.(
                                                                                                                                                                                                                                                                                                                                                                           US-08-159-339A-109
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US-08-482-228-187
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APPLICANT: Baldwin, David
APPLICANT: Baldwin, David
APPLICANT: Boxy, Datid W.
APPLICANT: Leaby, Ellen W.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
                                       Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22; DB 1; I
Pred. No. 2.4e+02;
1; Mismatches 1;
                                                                                                       FILING DATE: 01/FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATE: 02/FEB-1995
FILING DATE: 02-FEB-1994
CLASSIFICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
FELEPHONE: 415-496-2300
TELEFAX: 415-436-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/03465391A; Patent No. 5786331; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Barrett, Ronald W. APPLICANT: Yanofsky, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.0
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-383-474B-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||: ||
1 GSWEQP 6
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ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-465-391A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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0
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to the NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 1; Length 10;
Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides and Compounds That Bind to
the IL-1 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,788A
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                          Affymax Technologies N.V
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Patent No. 5/67234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEPAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                            4001 Miranda Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%;
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Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                                                                                                                                                                               STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GSFTQP 8
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1 GSWEQP 6
                                                                                                                                                                                          ADDRESSEE:
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US-08-383-474B-69
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APPLICANT: APPLICANT: Ranald W.

APPLICANT: Pareft, Ronald W.

APPLICANT: TITLE OF INVENTION: IL-1 Receptor

TITLE OF INVENTION: IL-1 Receptor

NUMBER OF SEQUENCES: 392

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22; DB 2; Len
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREEF: Two Embarcadero Center, Bighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                             Score 22; DB 2; 1
Pred. No. 2.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16528A-001850US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORREY AGENT INFORMATION:
NAME: SNYder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 1652/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                   94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%;
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Best Local Similarity 66./۰
اجم 4; Conservative
                                                             10 amino acids
                                                                                                                                                                                                             Query Match 40.0
Best Local Similarity 66.7
Matches 4; Conservative
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                       TYPE: maino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-463-076E-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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94111-3834
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| GSWEQP 6
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                                                             LENGTH:
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APPLICANT: Baldwin, David
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillipe R.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 1; Length 10; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5786331viel, Vern
RECISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/08464538B Patent No. 5861476
                                                                                                                                              TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen
                                                                                                                                                                                                                                                                                                                                                               40.0%;
02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                              Query Match 40.0
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-465-391A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcad
CITY: San Francisco
STATE: California
COUNTRY: USA
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1 GSWEQP 6
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Gaps
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Fatent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tsenq-Law, Janet
APPLICANT: Robori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgerson, Sam L.
APPLICANT: Boans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guitrie, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.2%; Score 21; DB 2; Length 6; 80.0%; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: 1T-4630CIP3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 8:
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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REGISTATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/482,528 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-228-8
                                                                                                                                COMPUTER READABLE FORM:
                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                       RY: USA
92713-5210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Irvine
                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TDGSF 5
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US-08-482-528-8
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CALF: 34939

CALF: SADSO

CAMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 5.25 INCH, 1.2 MB FOR FORMATTED
COMPUTER: IBM PC COMPATIBLE
OFBRATING SYSTEM: DOS
SOFTWARE: WORDPERECT 5.1
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11127
FILING DATE: NONE
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Helgerson, Sam L.
PAPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSTITUE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB 4; Length 10;
Pred. No. 2.4e+02;
2; Mismatches 4; Indels
                    Sequence 9, Application PC/TUS9511127
GENERAL INFORMATION:
APPLICANT: ROBERT WEBBER
APPLICANT: ROBERT WEBBER
TITLE OF INVENTION: DOPAMINE RECEPTOR PEPTIDES AND
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          ADDRESSE: BIELEN, PETERSON & LAMPE
STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720
CITY: WALNUT CREEK
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DENTIFICATION METHOD: AMINO ACID ANALYSIS

OTHER INFORMATION: DOPAMINE D2 RECEPTOR PEPTIDE
PCT-US95-11127-9
                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: D2 RECEPTOR (Ac-25-34)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08482228
Patent No. 5588753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: KODOTI, Joan A.
APPLICANT: Al-Abdaly, Fehad A.
APPLICANT: Al-Abdaly, Fehad A.
APPLICANT: Guillermo, Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.0
Matches 4; Conservative
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CORRESPONDENCE ADDRESS:
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1 SDGKADRPHY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
PCT-US95-11127-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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; ORCANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-100
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-173-941-100
| Sequence 100, Application US/09173941
| Patent No. 6140081
| GENERAL INFORMATION:
| APPLICANT: BARBAS, CATIOS F.
| TITLE OF INVENTION: 2INC FINGER BINDING DOMAINS FOR GNN FILE REFERENCE: NOV0081S
| CURRENT APPLICATION NUMBER: US/09/173,941
| UNBER OF SEC ID NOS: 120
| SOFTWARE: Patentin Ver. 2.1
| LENGTH: 7
| LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 38.2%; Score 21; DB 3; Length 7; Best Local Similarity 57.1%; Pred. No. 1.3e+05; Matches 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                   Query Match 38.2%; Score 21; DB 3; Length 6; Best Local Similarity 80.0%; Pred. No. 1.3e+05; Matches 4; Conservative 0; Mismatches 1; Indels
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
GS-08-482-528-8
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 17, 2001, 13:40:06 Run on:

// Search time 43.61 Seconds
(without alignments)
7.057 Million cell updates/sec

US-08-765-837-4 48 Title: Perfect score:

1 NQASRPYSF 9 Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

268485 seqs, 34193795 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_ Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

tesult No. S 1 2 3 4	Score 48 33 31 31	Query Match 100.0 68.8 64.6 64.6	Query Match Length DB 100.0 68.8 64.6 7 10 64.6 7 10 64.6 7 10	DB 17 18 10 10	ID R90048 W32492 P90351 W32A334	Description Factor VIII antige Helicostatin 3, wh Peptide fragment o Peptide fragment o
	29	60.4	, r r	15	R62417 W32499	Dipteran neuropepe
	27	56.2	· œ	18	W32506	Pteridostatin 2, w
	27	56.2	σ	20	Y47047	Immunogenic peptid
	25	52.1	7	10	P90859	New bradykinin ana
	25	52.1	σ	21	Y55007	Mouse histocompati
	24	50.0	σ	15	R71753	Neurotensin recept

Membrane dipaptida Neurotensin recept HIA binding plu-1 Mouse anti-11-18 a N. denitrificans a	Antigenic peptide Heat shock protein New substrate 3 fo Cytoskeleton local Local isation slona	Peptide which mimi Anti-cancer specif HLA binding plu-1 Neuropeptide repre	C.vomitoria allato Antigenic peptide Antigenic pertide Antigenic peptide Suntigenic citata	chrome citrate neurope ia alla	statin nic uci lhypert er amyl	Timothy grass poll Timothy grass poll NPF moth! EH domai BCT-Abl epitope (a
Y48827 R71755 Y55541 Y44591 W90991	Y01578 Y16921 P81974 R48278 W96376	Y54429 W16655 Y55540 R49938	R83634 Y01575 Y01576 Y01565	W93248 W93248 Y80302 R62418 R83632 R98051		W30959 W30993 W83248 Y53343
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ALIGNMENTS

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(first entry)

88EP-0310801.

87US-0121217

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ww polypeptide fragments
useful for neutralising activity of Factor 8 inhibitor.
                                                                                                                                                                                 Peptide fragments; human factor 8; Factor 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; page 3 and page 6; 7pp; English.
                                                                                                                                                     Peptide fragment of human factor 8.
                                                                                                                                                                                                                                                                                                                                                 (SCRI ) SCRIPPS CLINIC RES.
                                                                    P90351 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                            Zimmerman TS, Fulcher
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                                                                                                                          01-NOV-1989
                                                                                                                                                                                                            Homo sapiens
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  1 srpysf
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Matches
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           Peptides R90945-64 are derived from the factor VIII protein, esp. from a modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to von Willebrand factor, esp. antibodies, thus preventing or treating immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                 Blowfly; callatostatin; insect neuropeptide; Leu-callatostatin; gut motility; cockroach; insecticide; blowfly; cydiastatin; helicostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a specifically claimed callatostatin-
like peptide which is active as an inhibitor of gut motility. The
callostatin-like peptides can be used as insecticides, particularly
against lepidopteran insects. The invention relates to novel recombinant
or isolated DNA sequences representing the Helicoverpa armigera
helicostatin gene, the DraI fragment from Calliphora vomitoria or the
Lucilia cuprina prohomone coding sequence. These sequences encode
proteins of 228, 177 and 179 amino acids respectively.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New callatostatin-like peptide(s) and DNA - are active as inhibitors of gut motility, used as insecticides, particularly against lepidopteran insects
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                                                                                                                                                                                                                                                                                                                                                                                       Helicostatin 3, which inhibits gut motility in the blowfly.
                                                                                                                                                   100.0%; Score 48; DB 17; Length 9; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (QUEE-) QUEEN MARY & WESTFIELD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 62; 92pp; English.
                                                                                                                                                                                                                                                                                                      W32492 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            East P, Johnsen AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96GB-0006272.
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                                                                                                                                                                                                                                                                                                                                                             21-APR-1998 (first entry)
                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicoverpa armigera
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                                                                                                           9 AA;
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Peptide fragment of human factor 8, which neutralises the activity of the factor 8 inhibitor. Corresponds to residues 466-472 of factor 8 reported by 'Structure of human factor VIII' Nature Vol 312: 337-342 (1984).
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                                                                                                         % Score 31; DB 10; Length 7; Similarity 100.0%; Pred. No. 2.1e+05; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                               Peptide fragments; human factor 8; Factor 8.
                                                                                                                                                                                                                                                                                                                                     Peptide fragment of human Factor 8.
                                                                                                                                                                                                                                                       7 AA.
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                                                                                                                                                                                                                                                      P90354 standard; protein;
                                                                                                                       Local Similarity
                                                                   7 AA;
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                                                                                                                                                                                  2 ngasrp 7
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The sequences given in R62414-18 are neuropeptides derived from the blowfly, calliphora vomitoria. The peptides are extracted either from whole bodies or heads or C. vomitoria, or may be prepared by standard peptide synthesis. The peptides, called callatostatins, inhibit production of juvenile hormone (JH), which plays a crucial role in insect development by controlling metamorphosis, adult sexual maturity and reproduction. Callatostatin is the most powerful and inhibitor known for cockroaches, with max. inhibition at 1 nm and ED50 at 0.1 nm. The peptides can be used for insect control
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        edety
                                                                                                                                                                                                                                                                                                                                     Neuropeptide; blowfly; C. vomitoria; callatostatin; inhibition; juvenila hormone; JH; insect development; metamorphosis; adult sexual maturity; reproduction; insect control; environmentally friendly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diptera neoropeptide(s), partic. from blowfly Calliphora vomitoria - are juvenile hormone prodn. inhibitors, used for insect control, partic. cockroaches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15; Length 7; 2.1e+05;
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                                                        Score 30; DB 18; La Pred. No. 2.1e+05; 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                         Dipteran neuropepetide, callatostatin 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 7; 11pp; English.
                                                                                                                                                                                                                     R62417 standard; Protein; 7 AA.
                                                         62.5%;
83.3%;
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                                                                                      5; Conservative
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Matches 5; Conserve
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                                                        Query Match
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               8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a specifically claimed callatostatin-
like peptide which is active as an inhibitor of gut motility. The
callostatin-like peptides can be used as insecticides, particularly
against lepidopteran insects. The invention relates to novel recombinant
or isolated DNA sequences representing the Helicoverpa armigera
helicostatin gene, the Draf fragment from Calliphora vomitoria or the
fucilia cuprina prohomone coding sequence. These sequences encode
proteins of 228, 177 and 179 amino acids respectively.
                                                                                                                                                                                     Peptide fragment of human factor 8, which neutralises the activity of the factor 8 inhibitor. Corresponds to residues 1776-1782 of factor 8 reported by 'Structure of human factor VIII' Nature Vol 312: 337-342 (1984).
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New callatostatin-like peptide(s) and DNA - are active as inhibitors of gut motility, used as insecticides, particularly against lepidopteran insects
                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicostatin 4, which inhibits gut motility in the blowfly.
                                                                                                              New polypeptide fragments
- useful for neutralising activity of Factor 8 inhibitor.
                                                                                                                                                                                                                                                                                                       64.6%; Score 31; DB 10; Length 7; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                          Claim 2; page 3 and page 6; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thorpe A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (QUEE-) QUEEN MARY & WESTFIELD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 62; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W32493 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             East P, Johnsen AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-GB00843.
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87US-0121217
                           (SCRI ) SCRIPPS CLINIC RES
                                                      Zimmerman TS, Fulcher CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicoverpa armigera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-489644/45.
                                                                                   WPI; 1989-179956/25.
                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                             7 AA;
                                                                                                                                                                                                                                                                                                                                                                  1 NQASRP 6
                                                                                                                                                                                                                                                                                                                                                                                             2 ngasrp 7
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16-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-0CT-1997
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W32493;
                                                                                                                                                                                                                                                                                                                                                                                                                                         n
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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W32499;

RESULT W32499

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The present sequence represents a specifically claimed callatostatin-like peptide which is active as an inhibitor of gut motility. The callostatin-like peptides can be used as insecticides, particularly against lepidopteran insects. The invention relates to novel recombinant or isolated DNA sequences representing the Helicoverpa armigera helicostatin gene, the Drai fragment from Calliphora vomitoria or the Lucilia cuprina prohomone coding sequence. These sequences encode proteins of 228, 177 and 179 amino acids respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic peptide having a human leukocyte antigen binding motif #1.658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                      active as inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Southwood S;
                                                                                                                                                                                                                                                                                    New callatostatin-like peptide(s) and DNA - are active as in of gut motility, used as insecticides, particularly against lepidopteran insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 18; Length 8;
Pred. No. 2.1e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                             Thorpe A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sette A, Kubo RT, Sidney J, Celis E,
                                                                                                                                                                                                                                                                                                                                                                 Claim 25; Page 65; 92pp; English.
                                                                                                                                                                     (QUEE-) QUEEN MARY & WESTFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y47047 standard; Peptide; 9 AA.
                                                                                                                                                                                                           Johnsen AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.2%;
66.7%;
                                                                                            97WO-GB00843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; immunisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                 WPI; 1997-489644/45.
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Best Local Similarity
                                                                                                                                                                                                           Duve H, . East P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA;
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                 WO9735981-A1
                                                                                            26-MAR-1997;
                                                                                                                                26-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | : |
1 arpynf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1998;
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                                                       02-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                         Blowfly; callatostatin; insect neuropeptide; Leu-callatostatin; gut motility; cockroach; insecticide; blowfly; cydiastatin; helicostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blowfly; callatostatin; insect neuropeptide; Leu-callatostatin;
gut motility; cockroach; insecticide; blowfly; cydiastatin; helicostatin;
pteridostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a specifically claimed example of a callatostatin peptide which is active as an inhibitor of gut motility. The callostatin peptides can be used as insecticides, particularly against lepidopteran insects. The invention relates to novel recombinant or isolated DNA sequences representing the Helicoverpa armigera helicostatin gene, the DraI fragment from calliphora vomitoria or the Lucilia cuprina prohomone coding sequence. These sequences encode proteins of 228, 177 and 179 amino acids respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \prime callatostatin-like peptide(s) and DNA - are active as inhibitors gut motility, used as insecticides, particularly against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                   Callatostatin 6, which inhibits gut motility in the blowfly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pteridostatin 2, which inhibits gut motility in the blowfly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.4%; Score 29; DB 18; L
100.0%; Pred. No. 2.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New callatostatin-like peptide(s) and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             East P, Johnsen AH, Thorpe A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (QUEE-) QUEEN MARY & WESTFIELD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 64; 92pp; English.
                                                                   W32499 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W32506 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 97WO-GB00843
                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                  Calliphora vomitoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lepidopteran insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-489644/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pteronida salicis.
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rpysf 5
                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-1997;
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                                                                                                                                                                                                                                                                                                                      W09735981-A1
                                                                                                                                                21-APR-1998
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Duve H,

Sequence

W32506;

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RESULT W32506

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Gaps

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Caps

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Length 7;

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This sequence is a histocompatibility antigen binding peptide. The invention relates to a method for active vaccination against antiologous cells expressing transmembrane proteins comprises administering to a patient a vaccine composition comprising at least an immunogenic portion of the extracellular domain of the transmembrane protein, or a xenogenelic homolog thereof, coupled to or administered with a carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  effective to break tolerance to the transmembrane protein and a pharmaceutically acceptable adjuvant. The method of the invention is used to treat a variety of cancers, especially B cell Non-Hoddkin's lymphoma (NHL) and other B cell diseases such as chronic lymphocytic leukhemia, autoimmune disorders and B-cell regulatory disorders. The methou is also useful for treating diseases and conditions where administration of antibodies to transmembrane proteins has been shown to provide
                                                                                                                      It may be prepd. by conventional liq. - or solid-phase peptide synthesis methods. It is useful for treating local pain, inflammation and swelling, rhinitis, hypotension, asthma, arthritis, diarrhoea, irritable bowel syndrome, carcinoid syndrome, angina pain, and anaphylactic or septic shock. Pharmaceutical compsns. can be made with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel compositions and methods utilizing a humoral \text{immun}_{\hat{\sigma}} response to treat B cell Non-Hodgkin's lymphoma and other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Active vaccination; autologous cell; transmembrane protein; cancer; B cell Non Hodgkin's lymphoma; B cell disease; autoimmune disorder; chronic lymphocytic leukaemia; B-cell regulatory disorder; therapy; mouse; histocompatibility antigen
                         with D-aminoacid in 7 position, useful as bradykinin antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse histocompatibility antigen binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roberts W, Zelenetz AD;
                                                                                                                                                                                                                                                                                                                                                                       52.1%; Score 25; DB 10; 80.0%; Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12; 43pp; English.
     New peptide bradykinin analogues
                                                                      Claim 20; Page 41; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y55007 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                              7 AA;
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| rpfsf
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                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Y55007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             having a human major histocompatibility complex (MHC) class I (also peptides can blud to a specific HLA allele (i.e. HLA-A subtypes than aller of the manned in the immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly inportant in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) crayed to prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cyctoxic T cell response, by contacting a cyctoxic T cell with the peptide e.g. to produce CTLEs x vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
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                                               New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \,
                                                                                                                                                                     Y45390 to Y48214 represent specifically claimed immunogenic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 20; Length 9; Pred. No. 2.1e+05; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Claimed in claim 20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New bradykinin analogue with D-Phe.
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                                                                                                                   Claim 1; Page 92; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P90859 standard; protein; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-D-Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88WO-US02959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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WPI; 1999-551214/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-085400/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
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therapeutic benefits, and especially where the target is also capable of transducing or receiving a signal important for cell growth or function. While therapeutic regimens using anti-CD20 concepts are potentially effective for the treatment of B cell Non-Hodgkin's lymphoma, they are passive therapies that do not directly involve the immune system of the patient. Thus, these therapies may require continued administration of the therapeutic agent for efficacy, and do not provide any long term protection against recurrence. The present invention uses a humoral immune response against CD20 found in B cells. The method does not need long term administration of the therapeutic agent, and provides long term
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention concerns highly sensitive fluorescent probes which allow for rapid and precise characterisation of neurotensin receptor binding properties on whole cells. The probes are of formula R1-C(=X)-R in which R1 is is a fluorophore chosen from fluorescein, rhodamine, Blue fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin-type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu Specific sequences are given in R71745 - R71972. The R1-CX- acyl group is linked to the peptide via the
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below. Also this amino acid can be
substituted by Lys or Orn."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fluorescent markers for neurotensin receptors - useful for in vitro labelling of neurotensin receptors on cell surface and to isolate neurotensin-receptor expressing cells
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                                                                                                                                                                                       Score 25; DB 21; Length 9; Pred. No. 2.1e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Neurotensin; NT; receptor; probe; fluorescent.
                                                                                                                                                                                                                                                                                                                                                                                                      Neurotensin receptor fluorescent probe.
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                                                                                                                                                                                                                                                                                                                          R71753 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 5; 19pp; English.
                                                                                                                                                                                         52.1%;
66.7%;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                               protection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes peptides that selectivel; home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the ordan or tissue is selected from prostate, lung, skin, retina, pancreas, gnt, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). 144618 to 449066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.
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N-terminus in position 1. The N-terminal amino acid may also substd. by Lys or \ensuremath{\mathsf{Orn}} .
                                           The present sequence represents one of the claimed peptide sequences for R.
                                                                                                                                                                                                          Score 24; DB 15; Length 9; Pred, No. 2.1e+05; 11 Mismatches 2; Indels
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Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y48827 standard; Peptide; 8 AA.
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Best Local Similarity
                                                                                                                                    9 AA;
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conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                      Sequence
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New nucleic acid encoding the cancer-associated polypeptide plu-1, for diagnosis, treatment and prevention of cancer, especially of breast and
                                                                                                                                     Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine; breast cancer; immune response; cytotoxic T lymphocyte; imaging agent; therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                  (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
 Y55541 standard; peptide; 9 AA.
                                                                                                     HLA binding plu-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Taylor-papadimitriou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-591090/50.
                                                                                                                                                                                                                           Homo sapiens.
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The present sequence represents one of the claimed peptide
                                                                                                                                                                                                                                                                                                                         /note= "N-acylated with fluorescent label. See CC below. Also this amino acid can be substituted by Lys or Orn."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fluorescent markers for neurotensin receptors - useful for i
vitro labelling of neurotensin receptors on cell surface and to
isolate neurotensin-receptor expressing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.8%; Score 22; DB 15; Length 9; 57.1%; Pred. No. 2.1e+05; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                         Neurotensin; NT; receptor; probe; fluorescent.
                                                                                                                                                                                       Neurotensin receptor fluorescent probe.
                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                 R71755 standard; peptide; 9 AA.
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                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYMC-) UNIV MCGILL.
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                                                                                                                  R71755;
                                                RESULT 14
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98GB-0005877

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The invention relates to a human cancer-associated polypeptide plu-1. The plu-1 polypeptide can be recombinantly expressed by standard recombinant methodology. Detection of the plu-1 nucleic acid or the polypeptide is used for the following: (i) diagnosis (including immigne) and prognosis of and determination of susceptibility to, cancer, specifically ovarian or breast cancer cells, e.g. as a vaccine, or by inducing an immune response against cancer cells, e.g. as a vaccine, or by antisense inhibition). Antigens derived from the polypeptide are used to generate activated cytotoxic T lymphocytes, or dendritic cells, for subsequent return to the patient for treatment of cancer. The polypeptide may also be used to identify inhibitors of plu-1 activity. Fragments of the polypeptide, and antibodies raised against plu-1, are useful as assay and imaging agents, also therapeutically (to induce an anti-idiotype response or where computated to cytotoxic agents). The plu-1 antigen is expressed more computated to cytotoxic agents). The plu-1 antigens spreassed more computated to cytotoxic agents. The plu-1 antigens spreassed more computated to cytotoxic agents. The plu-1 antigens sequences yield the human class I alleles B27, A2, A3 and A11.
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Job time: 135 sec
Example 2; Fig 12; 173pp; English.
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

January 17, 2001, 13:41:26 ; Search time 58.21 Seconds (without alignments) 18.122 Million cell updates/sec Run on:

US-08-765-837-4

1 NOASRPYSF 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

374700 seqs, 117207915 residues Searched:

467 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_15:* Database

sp_archea:*
Sp_bacteria:*
Sp_fungi:*
Sp_human:*
Sp_invertebrate:*
Sp_mammal:* sp_vertebrate:*
sp_unclassified:* sp_organelle:* sp_rodent:* sp_virus:* sp_plant:* sp_phage: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P93233 lycopersico	098866 spinacia ol	Q67605 squash leaf	Q67606 squash leaf	Q63668 rattus norv	09r7t2 escherichia	Q9vvj2 drosophila	Q9twh6 perinereis	Q9trx8 bos taurus	Q50832 methanococc	Q53914 streptomyce	Q9ukj6 homo sapien	Q9tru7 bos taurus	Q66113 cherry leaf	Q9uj50 homo sapien	Q9t4y2 asterina pe	Q9qvd3 rattus sp.	P82598 rattus norv	O89965 polyomaviru
SUMMARIES		ai ai	P93233	998860	067605	067606	063668	Q9R7T2	Q9VVJ2	оэтмн6	Q9TRX8	050832	053914	Q9UKJ6	Q9TRU7	066113	Q9UJ50	Q9T4Y2	Q9QVD3	P82598	089965
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ALIGNMENTS

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Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euastr...ds 1;
Solanales: Solanaceae: Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97351561; PubMed-9207843;
Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
Differential induction of seven 1-aminocyclopropane-1-carbox, late synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum).";
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                                                                                                                                                                                                                                                                                                                       Plant Mol. Biol. 34:275-286(1997).
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE = 1-
AMINOCYCLOPROPANE.1-CARBOXYLLTE + METHYLTHIOADENOSINE.
-!- COFACTOR: PYRIDOXAL-PHOSPHATE.
EMBL; U75692; AAC49682.1; -.
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                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
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1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (EC 4.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                     1 1 7 AA; 828 MW; 71B412C7377415D0 CRC64;
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100.0%; Pred. No. 3.7e+05;
Live 0; Mismatches 0;
                             7 AA.
                             PRT;
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LE-ACS1B.
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Best Local Similarity 100.0
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                    Herrmann R.G.;
                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                       MEDLINE-86120353; PubMed=3003688; Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G. Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G. Spinach plastid genes coding for initiation factor IF-1, ribosomal protein S11 and RNA polymerase alpha-subunit."; Nucleic Acids Res. 14:1029-1044(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lazarowitz S.G.;
"Molecular characterization of two bipartite geminiviruses causing aguash leaf curl disease: role of viral replication and movement functions in determining host range.";
Virology 180:70-80(1991).
EMBL; M63155; AAA47823.1;
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                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYTCCHROME B/F SUBUNIT IV (FRAGMENT).
Spinacia oleracea (Spinach).
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10829;
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Pred. No. 3.7e+05;
1; Mismatches 0;
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MEDLINE=91082450; PubMed=1984669;
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(TrEMBLrel. 01, I
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Similarity 66.7%;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
A COMPONENT DNA (FRAGMENT).
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Best Local Similarity 75.0°,
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"Inverse PCR-mediated cloning of the promoter for the rat vasopressin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rartus.
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MEDLINE=91082450; PubMed=1984669;
Lazarowitz S.G.;
Molecular characterization of two bipartite geminiviruses causing squash leaf curl disease: role of viral replication and movement functions in determining host range.";
Virology 180:70-80(1991).
EMBL; M63157; AAA47822.1; -.
BMBL; M03157; AAA47822.1; -.
SEQUENCE 9 AA; 1118 MW; 2B30D5B457645417 CRC64;
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(FRAGMENT).
                                                                                       Squash leaf curl virus.
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
VCBI_TaxID=10829;
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Pflugers Arch. 430:12-18(1995).
EMBL; X83264; CAA58237.1;
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Best Local Similarity 75.0
Matches 3; Conservative
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Matches 3; Conservative
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RA Adams M. D., Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S. E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S. E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandrell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Briton R.C., Bayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., Derman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Morkulov G., Milshina N.V., Nobarry C., Morris J., Moshrefi A.,

Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                              Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                   "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding to the 12.7-28.0 min Region on the Linkage Map."; DNA Res. 3:137-155(1996).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Last annotation update)
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D90705; BAA35310.1; -.
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                           NCBI_TaxID=562;
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A She B.C., Siden Klamos I., Simpson M., Skropski M. F., Smilth T.,
A Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A. H., Wany X.,
A Wang Z.-Y., Wassarman D.A., Welnstock G.M., Welssenbach J. G.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao G.A.,
X Ye J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zhao O., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
A Libbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 28:2185-2195(2000).
R FLYBASE: FBgn0036743; CG6143.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantla; Pecora; Bovoídea;
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Phyllodocida; Nereididae; Perinereis.
NCBI_TaxID=6355;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
BIOACTIVE PEPTIDE P4-PUTATIVE ESOPHAGEAL NEUROREGULATOR.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
0STEOPONTIN.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
6AP-3, GTPASE-ACTIVATING PROTEIN.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                  AR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCHI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The purification of a Rapl GTPase-activating protein from bovine brain cytosol.";
J. Biol. Chem. 257:1546-1553(1992).
SEQUENCE 9 AA; 1063 MW; 89EDA77B47604B5A CRC64;
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Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
Burgess A.W.;
                                  0; Indels
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Pred. No. 3.7e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Zhang W., Li X.Q., Wu Q.F.:

"A splitce-site mutation in Androgen Receptor gene.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF159087; AAF04001.1:
   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 14; DB 6; Length 9; 100.0%; Pred. No. 3.7e+05; ive 0; Mismatches 0; Indels
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   29.2%; Score 14; DB 2; 140.0%; Pred. No. 3.7e+05; iive 3; Mismatches 0;
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Best Local Similarity 75.0%;
Matches 3; Conservative
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9 AA; 1272 MW;
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Matches 2; Conservative
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6 SRMY 9
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5 RAAQP 9
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MEDLINE-86230552; PubMed-4006907;
MEDLINE-96230552; Kuehn R., Klein A.;
Bollschweiler C., Kuehn R., Klein A.;
"Non-repetitive AT-rich sequences are found in intergenic regions of Methanococcus voltae DNA.";
EMBO J. 4:805-809(1985).
EMBL; X02518; CAA26355.1; -.
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Streptomyces cyaneus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1904;
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                                               Prince C.W., Dickie D., Krumdieck C.L.; "Osteopontin, a substrate for transglutaminase and factor XIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 3.7e+05;
2; Indels
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Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
EMBL; M33704; AAA26724.1; -.
NON_TER
SEQUENCE 9 AA; 1027 MW; 995BDDDDC4140AB1 CRC64:
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
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Last annotation update)
                                                                                activity.";
Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last anno
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                              MEDLINE=91282766; PubMed=1676261;
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Best Local Similarity 40.07
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Best Local Similarity 60.0*
"Thes 3; Conservative
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4 KPXXF 8
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TREMBLRel. 08, Last annotation update)
C-TERNINUS OF THE VIREA REPLICASE (FRAGMENT).
cherry leaf roll virus.
                                                                                                                                                                                                                                                                                                                        Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.; "Long, nearly identical untranslated sequences at the 3' terminal regions of the genomic RNAs of cherry leafroll virus (walnut strain)."; Virus Genes 10:245-252(1995).

EMBL; 234265; CAA84019.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White G.R.M., Varley J.M., Heighway J.; "Isolation and characterisation of a human homologue of the latrophilin gene from a region of 1p31.1 implicated in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.1%; Score 13; DB 12; Length 7; Best Local Similarity 60.0%; Pred. No. 3.7e+05; Matches 3; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
White G.R.M., Varley J.M., Heighway J.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ244509; CAB60204.1; -.
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAY-2000 (TrEMBLrel. 13, Last anno
LATROPHILIN-2 (FRAGMENT).
                                                                 PRT;
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MEDLINE=96124520; Pubmed=8560786;
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NCBI_TaxID=12615;
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Query Match 27.1%; Score 13; DB 4; Length 8;
Best Local Similarity 25.0%; Pred. No. 3.7e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps
Qy 4 SRPY 7
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Search completed: January 17, 2001, 13:44:40 Job time: 194 sec

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利力を発見している。 1975年の1975年の「現である」とは、1985年の19						

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:41:01; Search time 36.59 Seconds (without alignments) 16.701 Million cell updates/sec Run on:

US-08-765-837-4 48 1 NQASRPYSF 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

787 Total number of hits satisfying chosen parameters:

195891 seqs, 67900655 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР			COLUMNIC	
Result No.	Score	Query Match	Length	DB	ID	Description
1	29	60.4	8	. 7	D47393	neuropeptide calla
7	20	41.7	8	7	E47393	neuropeptide calla
e	17	35.4	σ	~	S70332	endosperm protein,
4	16	33.3	6	7	PC7076	spectrin alpha cha
2	15	31.2	9	7	151317	bHLH transcription
9	15	31.2	7	7	E33932	Ig mu chain D regi
7	15	31.2	8	7	PT0030	inulinase (EC 3.2.
8	15	31.2	80	7	PH0934	T-cell receptor be
6	15	31.2	σ	~	A61057	Thr-6 bradykinin -
10	15	31.2	6	7	A26744	bradykinin-like pe
11	15	31.2	6	~	A61363	bradykinin - commo
12	15	31.2	6	7	A60579	bradykinin-like pe
13	15	31.2	6	7	B60246	
14	15		σ	~	S65433	bradykinin - horn
15	15		σ	7	S78420 ·	ribosomal protein
16	15	31.2	σ	7	A43065	hydroxyproline-3-b
17	15		σ	4	S15594	orf 1 rara 5'-regi
18	14	29.5	ιO	~	JS0319	hage
19	14	29.5	S	~	PT0714	v
20	14	29.5	9	~	PT0618	T-cell receptor be
21	14	δ	9	~	PT0715	T-cell receptor be
22	14	6	7	-	A61324	
23	14	ė,		~	A60139	fatty-acid synthas
24	14			7	S36662	
25	14	σ		7	S21230	dermorphin (Trp-4,
56	14	9		7	S21288	lectin - potato (f
27	14	φ.	80	7	S66646	cardioacceleratory
28	14	29.5	æ	7	B45800	serum albumin - do
29	14	29.5	6	7	JS0302	xenopsin-related p

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Caps ; ;

1; Indels

Query Match
41.7%; Score 20; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels

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30 14 29.2 9 2 A60320 31 14 29.2 9 2 S30494 33 14 29.2 9 2 B44186 34 14 29.2 9 2 B7784 35 14 29.2 9 2 S17784 36 14 29.2 9 2 PH1591 37 13 27.1 6 2 PH0551 40 13 27.1 6 2 PF0652 41 13 27.1 6 2 PF0652 42 13 27.1 6 4 A55039 44 13 27.1 6 4 A55039 44 13 27.1 8 2 PF0651 45 13 27.1 6 2 PF0651 46 13 27.1 6 4 A55039	xenopsin related p	cat gene leader pe	chloramphenicol 0-	ATPase R1 subunit	cytochrome-c oxida	enamelin i - bovin	Ig H chain V-D-J ı	T-cell receptor be	T-cell receptor be	sperm acrosomal pr	T-cell receptor be	T-cell receptor be	hypothetical colla	T-cell receptor be	T-cell receptor be	T-cell receptor be
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	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 D47393
neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria) C;Species: Calliphora vomitoria C;Date: 16.Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C, ACCESSION: D47393 R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A. Broc Na+1 Acad Gri H.S. A 90, 2456-2460 1993
A.Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with seq. A:Reference number: A47393; MUID:93211980
A:Status: preliminary A:Status: preliminary
A.Residues: 1-8 cDUV> A.Experimental source: thoracic ganglia A.Note: sequence extracted from NCBI backbone (NCBIP:128479)
Query Match 60.4%; Score 29; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Hps 0;
Qy 5 RPYSF 9
 Db 2 RPYSF 6
 RESULT 2 E47393
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria) C; Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995 C;Accession: E47393
R; Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A. Proc. Natl. Acad. Sci. U.S.A. 90, 2455-2460, 1993
 A; Rittle: Callatostatins: neuropeptides from the blowfly Calliphora , witoria with seq. A; Reference number: A47393; MUID:93211980
A.Status: preliminary A.Moleule types protein
A; Experimental source: whole flies A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

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Gaps

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Treell receptor beta chain V-D-J region (clone 5) - rat (fragment)
C;Species: Rattus norvegicus (Norvay rat)
C;Date: 09-0ct-1992 #sequence_revision 09-0ct-1992 #text_change 30-May-1997
C;Accession: PH0934
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allem A;Reference number: PH0991; MUID:92078857
A;Accession: PH0934
                                                                                                                                                                                                                                                                Ig mu chain D region (E7) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: O9-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996 C; Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996 R; Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S. Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989 A; Title: Two murine natural polyreactive autoantibodies are encoded by noumutated ger A; Reference number: A33932; MuID:89282823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)
N;Alternate names: inulase
C;Species: Aspergillus ficuum
C;Species: Aspergillus ficuum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
C;Accession: PT0030
R;Ettallbi, M.; Baratti, J.C.
Agric. Biol. Chem. 54, 61-68, 1990
A;Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.
A;Reference number: PT0030; MUID:90344234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: PT0030
A;Molecule type: protein
A;Residues: 1-8 <ETT>
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                          1; Indels
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  Score 15; DB 2; Length
Pred. No. 2e+05;
2; Mismatches 1; Inde
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Pred. No. 2e+05;
1; Mismatches
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  31.2%;
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66.7%;
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Best Local Similarity 66./ 1
Query Match
Best Local Similarity 40.0
Matches 2; Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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A;Molecule type: mRNA
Residues: 1-7 <BAC>
A;Cross-references: GB:M27106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: immunoglobulin
                                                                                                         3 ASRPY 7
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1 RPF 3
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NA Alternate names: footin alpha chain
C;Species: Wus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000
C;Date: 18-Aug-2000
B;Stroygita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of the A;Reference number: PC7072
                                                                                                 endosperm protein, 10K - rye (fragment)

C;Species: Secale cereale (rye)

C;Species: Secale cereale (rye)

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C;Accession: S70332

R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.

B;Cohn. Biophys. Acta 1295, 13-22, 1996

A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.

A;Reference number: S70327; MUID:96283789
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151317
R;Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.
Mech. Dev. 50, 119-130, 1995
A;Title: 1d gene activity during Xenopus embryogenesis.
A;Reference number: 151316; MUID:95344988
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-6 <2HA>
A;Residues: 1-6 <2HA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Residues: 1-9 <TSU>
A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
C;Keywords: brain
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Pred. No. 2e+05;
1; Mismatches
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Pred. No. 2e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.4%;
50.0%;
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60.0%;
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Best Local Similarity 60.v.
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Best Local Similarity
'has 2; Conserve
                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ROC>
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1 NSATR 5
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Cycacesion: A60579
R;Conlon, J.M.; Hicks, J.W.; Smith, D.D.
R;Conlon, J.M.; Hicks, J.W.; Smith, D.D.
R;Conlon, J.W.; Hicks, J.W.; Smith, D.D.
R;Reference number: A60579; MUID:90126625
A;Molecule type: protein
A;Residues: 1-9 <CON>
A;Molecule type: protein
A;Residues: 1-9 <CON>
C;Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammali
C;Superfamily: unassigned animal peptides
C;Keywords: plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Firmura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.
Adv. Exp. Med. Biol. 247A, 359-367, 1989
Advi. Exp. Med. Biol. 247A, 359-367, 1989
A;Title: Ornithho-kininogen and ornithho-kinin: isolation, characterization and chemica A;Reference number: A60246; MUID:90102072
A;Accession: B60246
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 < KIM>
C;Superfamily: unassigned animal peptides
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C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Aug-2000
C;Accession: B60246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bradykinin-like peptide - slider turtle
C;Species: Pseudemys scripta (slider)
C;Date: 17-Apr.1993 #sequence_revision 17-Apr-1993 #text_change 18 And-2000
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                    RAnastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A.Title: Occurrence of bradykinin in the skin of Rana temporaria.
A.Reference number: A61363
A.Accession: A61363
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-9 <ANA>
C.Superfamily: unassigned animal peptides
C.Keywords: skin
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Pred. No. 2e+05;
0; Mismatches 2; Indels
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Pred. No. 2e+05;
0; Mismatches
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Pred. No. 2e+05;
0; Mismatches
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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  C; Accession: A61363
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                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Colpa interrupta
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Aug-2000
C;Accession: A61057
C;Accession: A61057
Comp. Biochem. Physiol. C 96, 157-162, 1990
A;Title: Threonine(6-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap
A;Reference number: A61057; MUID:91130217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: Thr-6-bradykinin
C;Species: Megascolia flavifrons (garden dagger wasp)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000
C;Accession: A26744
R:Yasuhara, T.: Mantel, P.: Nakajima, T.: Piek, T.
Toxicon 25, 527-535, 1987
A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary was
A;Reference number: A94322; MUID:87293024
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C:Species: Rana temporaria (common frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
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                                        A.Experimental source: complete Freund's adjuvant-immunized lymph node A.Note: the authors translated the codon CAG for residue 7 as Glu C.Keywords: T-cell receptor
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A;Residues: 1-9 <PIE.
C;Superfamily: unassigned animal peptides
C;Keywords: bradykinin; presynaptic neurotoxin; venom
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Pred. No. 2e+05;
0; Mismatches
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A;Residues: 1-9 <7AS>
C;Superfamily: unassigned animal peptides
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Best Local Similarity 60.0%;
Matches 3; Conservative
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Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
A; Molecule type: mRNA
A; Residues: 1-8 <GOL>
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Dradykinin - horn fly (fragment)
C.Species: Haematobia irritans (horn fly)
C.Species: Haematobia irritans (horn fly)
C.Species: Haematobia irritans (horn fly)
C.Species: Ba.Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C.Accession: S65433
R.Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, F. B.W. J. Blochen. 237, 414-423, 1996
A.Title: Cloning and characterisation of angiotensin-converting enzyme from the dipterant A.Feference number: S65431
A.Accession: S65433
A.Status: preliminary
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-9 <WIJ>
A.Note: the source is designated as Hacmatobia irritans exigua
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb_1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
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S. Graack, H.R.
Submitde to the Protein Sequence Database, February 1998
A. Reference number: S78411
A. Accession: S78420
A. Molecule type: protein
A. Residues: 1-9 <GOL>
A. Note: the protein is designated as mitochondrial ribosomal protein L41
C. Keywords: mitochondrion; protein biosynthesis; ribosome
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Pred. No. 2e+05;
0; Mismatches 2; Indels
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31.2%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 60.0%;
Matches 3; Conservative
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Search completed: January 17, 2001, 13:43:36 Job time: 155 sec

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OM protein - protein search, using sw model

January 17, 2001, 13:42:31; Search time 20.9 Seconds (without alignments) 13:907 Million cell updates/sec Run on:

US-08-765-837-4 48 1 NQASRPYSF 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

88757 seqs, 32294092 residues Searched:

213 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P82154 cydia pomon	P82155 cydia pomon		P81813 carcinus ma	P81818 carcinus ma	P81806 carcinus ma	P81807 carcinus ma	P81808 carcinus ma	P81819 carcinus ma	P81809 carcinus ma	P81811 carcinus ma	~	P41841 calliphora		P81820 carcinus ma	P81817 carcinus ma		P82156 cydia pomon	4	P43172 ascaris suu	P19991 acheta dome	P81805 carcinus ma	P99025 mus musculu	S	7	_	P81886 porphyromon	'n	4 staph	7	2 rattu	93	P82158 cydia pomon
SUMMARIES	ID	ALL3_CYDPO	ALL4_CYDPO	ALL4_CALVO	AL10_CARMA	AL15_CARMA	ALL3_CARMA	ALL4_CARMA	ALL5_CARMA	AL16_CARMA	ALL7_CARMA	ALL8_CARMA	ALL9_CARMA	ALL5_CALVO	FLA2_TREHY	AL17_CARMA	AL14_CARMA	AL18_CARMA	ALL5_CYDPO	AL11_CARMA	FAR9_ASCSU	SUGA_ACHDO	ALL2_CARMA	GFRP_MOUSE	AL12_CARMA	ALL1_CYDPO	ALL6_CYDPO	B44K_PORGI	COXE_THUOB	LPCA_STAAU	NEUX_HUMAN	NEUX_RAT	UPA7_HUMAN	ALL7_CYDPO
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	Result No.	1	7	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

	068928 salmon 11a			P19990 Leucophaea			054296 salm r 1 La		P42985 leptinetars		P25423 melolontha	P38644 mus musculu		
	RS10_SALTY	RS10_SERMA	UH11_RAT	LCK8_LEUMA	NPB_BOVIN	NEUU_CAVPO	RS11_SALTY	TKC1_CALVO	OVM_LEPDE	FARB_CALVO	AKH_MELML	UF06_MOUSE		ALIGNMENTS
	-	-	Н	Н	Н	-	н	-	٦	٦	7	-		
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1	27.1	27.1	25.0	25.0	25.0	25.0	25.0	25.0	22.9	22.9	22.9	22.9		
1	13	13	12	12	12	12	12	12	11	11	11	11		
;	34	35	36	37	38	39	40	41	42	43	44	45		

.u. 1 ALL3_CYDPO ALL3_CYDPO STANDARD: PRT; 8 AA. P82.154; 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)	Cydia pomonella (Codling moth). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Portricoidea; Portricidae; Olethreutinae; Cydia. SEQUENCE. TISSUE-LARVA; MEDLINE-98054539; PubMed-9392829; Duve H., Johnsen A.H., Maestro JL., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.; "Lepidopteran peptides of the allatostatin superfamily."; "Lepidopteran peptides of the ALLATOSTATIN FAMILY. Neuropeptide; Amidation. MOD_RES 8 AA; 926 MW; C82879D5AB477415 CRC64;	Y M Lo nes 1	TT 2 CYDPO STANDARD; PRT; 8 AA. BA114_CYDPO STANDARD; PRT; 8 AA. B2155; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 30-MAY-2000 (Rel. 39, Last annotation update) CYDIASTATIN 4. CYDIASTATIN 4. CYDIASTATIN 4. CYDIASTATIN 6. CYDIASTATIN 7. CYDIASTATIN 7. CYDIASTATIN 8. CYDIASTATIN 8. CYDIASTATIN 9. CYDIASTATIN 9. CYDIASTATIN 8. CYDIASTATIN 8. CYDIASTATIN 9. TOTATICOIDE 980054539; PubMed-9392829; MEDLINE-980054539; PubMed-9392829; DUVE H., JOHNSEN A.H., Meastro JL., SCOLT A.G., Winstanley I., Davey M., East P.D., Thorpe A.; Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).
ALL3_CYDPO ALL3_CYDPO ID ALL3_ DT 30-MA DT 30-MA DT 30-MA DF CYDIA		Query M Best Lo Matches Qy 4 Db 1	ALL4_CYDPO JAL14_CYDPO ALL4_CYDPO AC P8215_ DT 30-MA DT 30-MA DT 30-MA DT 30-MA DT CYDIA CYDIA COC PLETY COC C C C C C C C C C C C C C C C C C C

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30-MAY-2000 (Rel. 39, Last annotation update)
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Best Local Similarity
Matches 4; Conserv
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             CARCINUSTATIN 10
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| APQPYAF 7
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P81818;
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P81806;
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3 PYSF
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AL15_CARMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the blowfly calliphora vomitoria.";

Cell Tissue Res. 276:367-379(1994).

-I-FUNCTION: MAY ACT AS A NEURORANITTER OR NEUROMODULATOR AND PLAY

A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
BEHAVE AS POTENT INHIBITORS OF PERISTALIC MOVEMENTS. MAY ALSO
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.

-I-TISSUE SPECIFICITY: BRAIN, SUBDESOPHAGEAL GANGLION, RETROCEREBRAL
COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                         "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence homology to cockroach allatostatins."; Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Duve H., Thorpe A.; "Distribution and functional significance of Leu-callatostatins in
                                                                                                                                                                                                                                                                                                                                       MEDLINE-93211980; PubMed-8460157;
Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
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                                                                                 Indels
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                                                         Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.4%; Score 29; DB 1; Length 8; 100.0%; Pred. No. 8.9e+04; ive 0; Mismatches 0; Indels
                     922879D5AB47740D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AMIDATION.
954 MW; D32879D5AB47740A CRC64;
                                              Score 30; DB 1; Ler
Pred. No. 8.9e+04;
                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
31-ATCATATOSTATIN 4 (LEU-CALLATOSTATIN 4).
Calliphora vomitoria (Blue blowfly).
                                                                                                                                                                                     8 AA.
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(Rel. 39, Last sequence update)
                                                                                 1; Mismatches
            AMIDATION
                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94291167; PubMed-8020069;
                                                                                                                                                                                                             (Rel. 32, Created)
                                                      62.5%;
nilarity 83.3%;
Conservative 1
                     8 AA; 910 MW;
                                                                                                                                                                                                                                                                                                                            TISSUE=THORACIC GANGLION;
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Neuropeptide; Amidation.
                                                                                                                                                                                     STANDARD;
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                                                         Query Match
Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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P41840;
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SEQUENCE
                     SEQUENCE
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ID AL10_CP
AC P81813;
DT 30-MAY-
DT 33-MAY-
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Gaps
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-!- FUNCTION: MAY AGT. AS A NEUROTRANISMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-i-FUNCTION: MAY ACT AS A NEUROFFANSMITTER OR NEUROMODULATOR.
-i-SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide: Amidation; Multigene family.
MOD_RES
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                                                                                                                                                                      TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE=98121193; Pubmed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE=98121193; Pubmed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Carcinus maenas (Common shore crab) (Green crab).

Budaryota: Metazoa; Arthropoda; Cuutaceae; Malacostraca;

Bumalacostraca; Eucarida; Decapoda; Plecygemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eumalacostraca; Eucarida; Decapoda; Pléocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.1%; Score 25; DB 1; Length 9; 57.1%; Pred. No. 8.9e+04;
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 9 AMIDATION. 963 MW; 372D79CDCB4776C7 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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100.0%; Pre
0; )
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Matches 4; Conservative
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-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD_RES
                                                                                                                                                                                                                                                Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                                                                                                                   allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Blocohem. 250.727-734 (1997).
-1. FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATON.
-1. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multipene family.
7 7 AMIDATION.
SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;
                                                                                                                                                                                 MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carcinus maenas (Common shore crab) (Green crab).
Usukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
  30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 5.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Plecypemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.8%; Score 21; DB 1; Length 7; 75.0%; Pred. No. 8.9e+04; Live 1; Mismatches 0; Indels
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                                                                                                                                                                  TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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ID ALL7_CARMA STANDARD; F
AC P81809; P81810; P81804;
DT 30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.8
Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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3 PYSY 6
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ID AL16_CARMA
AC P81819;
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                                                                                                                                                                                                                                                            "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Multigene family.
SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
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                                                                                                                                                                                                                           Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                   CARCINUSTRYIN 3.

CARCINUSTRYIN 3.

CARCINUS maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Cutustaea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%; Score 21; DB 1; Length 7; 75.0%; Pred. No. 8.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION; MEDLINE-98121193; PubMed-9461295;
                                                                                                                                                                                   TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE-98121193; Pubmed-9461295;
30-MAY-2000 (Rel. 39, Last sequence update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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TD ALLS_CARMA
C P0180MY 2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
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Matches 3; Conserv
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PYAF 5
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P81807;
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Duve H., Johnson A.H., Scott A.G., East P., Thorpe A.;

"[Hyp3]Met-callatostatin. Identification and biological properties of a novel neuropeptide from the blowfly Calliphora vomitoria.";

J. Biol. Chem. 269:21059-21066(1994).

-!- FUNCTION: MAY ACT AS A NEUROTRANSHITER OR NEUROMODULATOR AND PLAY A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO BEHAVE AS POTENT INHIBITORS OF PERISTALIC MOVEMENTS. MAY ALSO FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
-!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calliphora vomitoria (Blue blowfly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda; Insecta;
Pterygota; Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridea; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence homology to cockroach allatostatins.";
Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CALLATOSTATIN 5 (MET-CALLATOSTATIN 1) ((HYP3)MET-CALLATOSTATIN)
                                                                                                                                                                                                                                                                                     "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).
                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
                                                                                                                                                                                                                                                 Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachywra;
                                                                                                                                                                                                                                                                                                                                                                                                        8 AA; 781 MW; 7C2879CDCB476878 CRC64;
                                                                                                                    Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                      TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE=98121193; PubMed=9461295;
                                                                                                                                                    Eumalacostraca; Eucarida; Decapoda; Pleocyemat:
Eubrachyura; Portunoidea; Portunidae; Carcinus
                                                   (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         Neuropeptide; Amidation; Multigene family.
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Best Local Similarity 75.0
Matches 3; Conservative
                         STANDARD;
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                                                                                                      CARCINUSTATIN 9
                                                     30-MAY-2000
30-MAY-2000
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                       ALL9_CARMA
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P41841;
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ALL5_CALVO
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                                                                                                                                                                                                                                  allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 256:727-734 (1997).
-11. FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 7 [CONTAINS: CARCINUSTATIN 6; CARCINUSTATIN 1].
CARCINUS maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                MEDLINE-98121193; Pubmed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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                                                                                   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                  "Isolation and identification of multiple neuropeptides
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3. 8.9e+04;
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CARCINUSTATIN 6.
CARCINUSTATIN 1.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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PYAF 6
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P81811;
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PYAF
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SEQUENCE
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Gaps

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Indels Length 8;

Pred. No. 8.9e+04; 1; Mismatches 0;

8 AA.

PRT;

Neuropeptide; Amidation; Hydroxylation.

PIR; E47393; E47393

RESULT, 12

Score 21; DB 1;

AMIDATION

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01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FLAGELLAR FILAMENT OUTER LAYER PROTEIN FLAA2 (35 KDA SHEATH PROTEIN)
 HYDROXYLATION (IN 20% OF THE PEPTIDES)
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MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARCINISTATIN 17.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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                                                   Score 20; DB 1; Length 8; Pred. No. 8.9e+04;
                                                                                                                                                                                                                                               Treponema hyodysenteriae (Serpulina hyodysenteriae)
Bacteria; Spirochaetales; Spirochaetaceae; Brachyspira
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                    7D9879CABB477768 CRC64;
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AL17_CARMA

ID AL17_CARMA STANDARD; PRT; 8 AA.
P81820;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                9 AA
                                                                       0; Mismatches
           AMIDATION
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8 8
8 AA; 883 MW;
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Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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3 PYDF 6
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SEQUENCE
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LOCATION: 8
OTHER INFORMATION: /product- "OTHER"
OTHER INFORMATION: /note- "C-terminal amide"
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                      RY: US
20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                    US-08-522-326-10
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
9, Appli
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1, Appli
1, Appli
6, Appli
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55, Appl
11, Appl
16, Appl
1, Appli
3, Appli
                                                         Search time 31.16 Seconds (without alignments) 5.187 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Ap Sequence 7, Ap Sequence 47, A Sequence 47, A Sequence 47, P Sequence 47, P Sequence 3, Ap Sequence 11, Sequence 16, Sequence 11, A Sequence 287, Sequence 287, Sequence 287, Sequence 287, Sequence 287, Sequence 287, Sequence 288
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Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                              US-08-522-326-10
US-08-522-326-15
US-08-773-190-47
US-08-373-190-47
US-08-373-190-47
US-08-38-190A-47
US-08-38-190A-47
US-08-287-145A-47
S49463-15
US-08-194-981E-65
US-08-194-198-188
US-08-194-198-188
US-08-194-198-188-188
US-08-194-198-188-188
US-07-920-878-11
US-07-920-878-11
US-07-920-878-11
                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                         174772 segs, 17957048 residues
                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                          January 17, 2001, 13:40:21

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 9
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                         Sequence 13, A Sequence 13, A Sequence 110, Sequence 111, Sequence 111, Sequence 17, A
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     Sequence
                Sequence
US-07-920-878-32
US-07-920-878-33
US-08-0878-33
US-08-014-979-11
US-08-014-979-110
US-08-014-979-111
US-08-218-608-1
US-08-672-805-18
US-08-776-613-2
US-08-776-613-5
US-08-776-613-5
US-08-776-613-5
US-08-776-613-6
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ALIGNMENTS

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OPERATING SISTEM: PC-LUS/MS-LUS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,326
FILING DATE: 12-SPP-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9305120.9
FILING DATE: 12-MRR-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUDWIG, STEVEN R.
REGISTRATION NUMBER: 36.203
REFERENCE/DOCKET NUMBER: 0623.0340000
TELECHONE: (202) 371-2600
TELECHONE: (202) 371-2600
TELECHONE: (202) 371-2600
TELECHONE: (202) 371-2600
SEQUENCE CHARACTERISTICS:
LENGTH: B amino acids
                                                                                                                                                                                                      STREET: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 STATE: D.C. STATE: D.C.
                                                                           APPLICANT: THORPE, Alan
APPLICANT: DVVE, Hanne
APPLICANT: DVVE, Hanne
APPLICANT: JOHNSEN Anders Holten
TITLE OF INVENTION: NEUROPEPTIDES AND THEIR USE ,
TITLE OF INVENTION: INSECTICIDES
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Calliphora vomitoria
Sequence 10, Application US/08522326
Patent No. 5753615
GENERAL INFORMATION:
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Gaps
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OTHER INFORMATION: /note= "Amidated leucine residue at OTHER INFORMATION: position 8"
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                                       APPLICANT: Duve, Hanne
APPLICANT: Thorpe, Alan
APPLICANT: Johnsen, Anders H.
TITLE OF INVENTION: Insect Neuropeptides
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESS: STEER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.4%; Score 29; DB 2; 100.0%; Pred. No. 1.3e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00505
FILING DATE: 09-MAR-1995
APPLICATION NUMBER: WO PCT/GB95/00505
FILING DATE: 09-MAR-1995
PRIOR APPLICATION NUMBER: GB 9404529.1
FILING DATE: 09-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32, 893
REGISTRATION NUMBER: 32, 893
REGISTRATION NUMBER: 32, 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. ....
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PATCHILI Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/714,053 FILING DATE: 09-SEP-1996 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Calliphora vomitoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.STICS:
LENGTH: 8 amino acids
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                        STREET: 1100 New CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09 CLASSIFICATION:
                                                                                                                                                                                                                                                         USA
  5863763
                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-373-190-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATION SYSTEM: PC-LOS/MS-LOS
SOFTWARE: PACEDIA #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,326
FILING DATE: 12-SPE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/520,326
FILING DATE: 12-MR-1993
APPLICATION NUMBER: GB 9305120.9
FILING DATE: 12-MR-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUDWIG, STEVEN R.
REGISTRATION NUMBER: 0623.0340000
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2540
INPORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: THORPE, Alan
APPLICANT: THORPE, Hanne
APPLICANT: DUVE, Hanne
APPLICANT: JOHNSEN, Anders Holten
ATTLE OF INVENTION: INSERTICIBES
TITLE OF SEQUENCES: 1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.4%; Score 29; DB 1; Length 8; 100.0%; Pred. No. 1.3e+05; Live 0; Mismatches 0; Indels
                                                                                                                           Length 8;
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Pred. No. 1.3e+05;
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
WO 94/20530 A2
                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/08522326 Patent No. 5753615 GENERAL INFORMATION:
                   ; FILING DATE: 14-MAR-1994
; PUBLICATION DATE: 15-SEP-1994
US-08-522-326-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 7, Application US/08714053
                                                                                                                           60.4%; 8
                                                                                                                         Query Match 60.4 Best Local Similarity 100. Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Chas 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-522-326-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20005-3934
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2 RPYSF 6
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US-08-714-053-7
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APPLICANT: RICHARDSON, JENNIFER
TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 2; Length 8;
Pred. No. 1.3e+05;
1; Mismatches 1; Indels'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORREY AGENT INFORMATION:
NAME: ELSENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956-CP3
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%; Score 21;
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/08350215 Patent No. 6004940 GENERAL INFORMATION:
                                                           TLIND CALE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, FONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-5440
TELERAX: (617) 523-5440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 47: SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.8%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                        US-08-438-190A-47
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US-08-350-215-47
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Batent No. 5965371
GENERAL INFORMATION:
APPLICANT: HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 2; Length 8;
Pred. No. 1.3e+05;
1; Mismatches 1; Indels
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PatentIn Release #1.0, Version #1.25
                     ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN STREET: 130 WATER STREET
STREET: BOSTON
STATE: MA
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,190
FILING DATE: 17.-JAN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US93/06735
FILING DATE: 16.-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESURCK, DAVID S
REGISTRATION NUMBER: 34,235
REFIERBANCE/DOCKET NUMBER: 41956-PCT-US
TELECAMOUNICATION INFORMATION:
TELECAMOUNICATION SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: US-08-373-190-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 43.8
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MASSACHUSETTS
COUNTRY: US
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NQASRP 6
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US-08-438-190A-47
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,053 FILING DATE: 09-SEP-1996 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                    Score 20; DB 5;
Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION 530
PRIOR APPLICATION 530
PRIOR APPLICATION 1948ER: PCT/GB95/00505
FILING DATE: 09-MAR-1995
APPLICATION NUMBER: WO PCT/GB95/00505
FILING DATE: 09-MAR-1995
FILING DATE: 09-MAR-1995
APPLICATION NUMBER: GB 9404529.1
FILING DATE: 09-MAR-1994
ATTONEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Duve, Hanne
APPLICANT: Thorpe, Alan
APPLICANT: Johnsen, Anders H.
TITLE OF INVENTION: Insect Neuropeptides
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0623.0430000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Calliphora vomitoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08714053 Patent No. 5863763
                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 954,418
FILING DATE: 30-SEP-1992
APPLICATION NUMBER: 496,800
FILING DATE: 21-MAR-1990
APPLICATION NUMBER: 812,796
FILING DATE: 23-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                      41.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                     FILING DATE: 02-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20005
                                                                                                                                                                        ; SEQ ID NO:15:
; LENGTH: 4
5494663-15
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1 PFSF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                           Gaps
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APPLICANT: YAMADA, MASAAKI; FURUTANI, YASUJI; YAMAYOSHI, MICHIKO; NOTAKE, MITSUE; VAMAGISHI, JUNICHI
INTEUE; VANAGISHI, JUNICHI
INTERLEUKIN 1 POLYPEPTIDES
NUMBER OF SEQUENCES: 34

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,826
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Patent No. 6072036
GENERAL INFORMATION:
APPLICANT: HARARSCO, WAYNE
APPLICANT: HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,145A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 3; Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-6440
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%;
                     66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 WATER STREET CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: US
                   Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 43.8
Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                           1 NQASRP 6
                                                                                                              2 NEASYP 7
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2 NEASYP 7
                                                                                                                                                                                   US-09-287-145A-47
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5494663-15
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/08/522,326
FILING DATE: 12-SEP-1995
FILING DATE: 12-SEP-1995
FILING DATE: 12-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUDDWIG: STEVEN R.
RECISTRATION NUMBER: 36,203
FELEPHONE: (202) 371-260
TELEPHONE: (202) 371-260
TELEPHONE: (202) 371-2540
INFORMATION FOR SEG ID NO: 11:
SEQUENCE CHARACTERISTICS:
THANGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.7%; Score 20; DB 1; Length 8; 75.0%; Pred. No. 1.3e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                    APPLICANT: THORPE, Alan
APPLICANT: DUVE, Hanne
APPLICANT: DUVE, Hanne
APPLICANT: JOHNSEN, Anders Holten
TITLE OF INVENTION: NEUROPEPTIDES AND THEIR USE AS
TITLE OF INVENTION: INSECTICIDES
UNUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 8
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER: WO 94/20530 A2 FILING DATE: 14-MAR-1994
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Patent No. 5753615
GENERAL INFORMATION:
APPLICANT: THORPE, Alan
APPLICANT: DUVE, Hanne
                                            Sequence 11, Application US/08522326
Patent No. 5753615
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Calliphora vomitoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FILING DATE: 14-MAR-1994
; PUBLICATION DATE: 15-SEP-1994
US-08-522-326-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                              ADDRESSEE: STERNE, KES
STREET: 1100 NEW YORK
CITY: HASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
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                         US-08-522-326-11
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Indels
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41.7%; Score 20; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                          Score 20; DB 2; Length 6; Pred. No. 1.3e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUO, ZUYU
APPLICANT: SANDHU, PUNAM
APPLICANT: GILLAM, Elizabeth M. J.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVENTION: CYTOCHROME P450
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
FILING DATE: FEDTUARY 10, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: NEEDLE FROSENBERG, P.C.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Selby
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0022
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Application US/08194981E Patent No. 5886157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                          Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
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US-08-194-981E-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                             6 PYSF 9
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| PYDF 4
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APPLICANT: Thorpe, Alan
APPLICANT: Johnsen, Anders H.
TITLE OF INVENTION: Insect Neuropeptides
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amidated methionine residue
at position 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 2; Length 8;
Pred. No. 1.3e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
LOCATION: 2
OCHER INFORMATION: /note= "Hydroxyproline residue at
OTHER INFORMATION: position 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-SEP-1996
CLASSIFICATION: 530
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00505
FILING DATE: 09-MAR-1995
APPLICATION NUMBER: WO PCT/GB95/00505
FILING DATE: 09-MAR-1995
FILING DATE: 09-MAR-1995
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: GB 9404529.1
FILING DATE: 09-MAR-1994
ATTORNEY/ABOTT INFORMATION:
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 32,893
FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371.2500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARRACTERISTICS:
LENGTH: B amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Calliphora vomitoria
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 8, Application US/03714053; Patent No. 5863763; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site LOCATION: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
'-has 3; Conserv?
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3 PYDF 6
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US-08-714-053-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-714-053-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
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                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/522,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Duve, Hanne
APPLICANT: Thorpe, Alan
APPLICANT: Thorpe, Alan
APPLICANT: Tohnsen, Anders H.
TITLE OF INVENTION: Insect Neuropeptides
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Mashington
                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
               TITLE OF INVENTION: NEUROPEPTIDES AND THEIR USE AS TITLE OF INVENTION: INSECTICIDES NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: LUDWIG, STEVEN R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0623.0340000
TELECOMMUNICATION INFORMATION:
TELEPHAX: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/522,326
FILING DATE: 12-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9305120.9
FILING DATE: 12-MAR-1993
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/714,053
FILING DATE: 09-SEP-1996
JOHNSEN, Anders Holten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08714053
Patent No. 5863763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-522-326-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Lase 3; Conserva
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                                                                                                                                                                                       COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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COUNTRY: US
ZIP: 20005
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3 PYDF 6
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Score 20; DB 1; Length 9;
Pred. No. 1.3e+05;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: January 17, 2001, 13:42:56 Job time: 155 sec
           NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFRENCE/DOCKET NUMBER: 1019.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAR: 415-424-0832
INFORMATION FOR SEQ ID NO: 287:
SEQUENCE CHARACTERISTICS:
LENTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.78;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.09
Matches 3; Conservative
                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                    NAME/KEY: Region LOCATION: 3
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3 AQPYS 7
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US-08-190-788A-287
Sequence 287, Application US/08190788A
Patent No. 5608035
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Balratt, Ronald W.
APPLICANT: Baldwin, David W.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to the TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies N.V.
STREET: 4001 Miranda Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "Amidated methionine residue orHER INFORMATION: at position 8" US-08-714-053-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.7%; Score 20; DB 2; Length 8; Best Local Similarity 75.0%; Pred. No. 1.3e+05; Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/190,788A
FILING DATE: 02-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00505
FILING DATE: 09-MAR-1995
APPLICATION NUMBER: WO PCT/GB95/00505
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9404529.1
FILING DATE: 09-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: BERNOIN, RODERT W.
RECISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0430000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-WAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Calliphora vomitoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
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3 PYDF 6
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; Search time 14.14 Seconds
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16.928 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35323
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268485 seqs, 34193795 residues
                                                                                                                                                                                                                                                                                                     January 17, 2001, 13:43:01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-765-837-7
43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Factor VIII antige	Protease-non-labil	Peptide #30 having	Opioid peptide. S	Anti-adherence pep	Anti-adherence pep		Anti-adherence pep	Anti-adherence pep	Anti-adherence pep	Anti-adherence pep	New peptide which
SUMMARIES	R90951	R38120	W43253	W28886	W15206	W15207	W15208	W15209	W15210	W15211	W15212	R93744
DB	17	14	19	18	18	18	18	18	18	18	18	18
% Query Match Length DB	7	4	4	9	9	9	9	9	9	9	9	9
% Query Match	100.0	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8
Score	43	24	24	24	24	24	24	24	24	24	24	24
Result No.	п	8	m	4	Ŋ	9	7	80	6	10	11	12

Claim 8; Page 31; 45pp; French.

Leader sequence 50 Opiold peptide whi Leader sequence 51 Leader sequence 12 Fourmale virus inhi Membranc dloerida	Immunomodulatory p Opioid peptide. S New peptide which Opioid peptide which	nonzod poly -18 r kin-l	Pentament commotop Control peptide fo Control peptide fo Endocarditis speci G30 sub domain of Low density lipopr Isselectric focusi Objoid mentide ss		
W40931 Y22992 W40932 W40893 W40893	W28978 W24339 W24339	Y83833 Y30217 W63815 Y39794 R12731	R69963 R98709 R79636 Y33848 W22916 W78366	W28133 W23133 R93748 W03277 W66594 Y25854	768864
19 19 19 20	17 18 18 20	20 12 12 12 12	16 17 18 20 18 18	70 70 70 70 70 70 70	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
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2 2 2 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4	3 3 3 3 3 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6	22 22 22 22 22 22	222222222222	222222	2112221222
13 14 15 17	19 20 21 22	23 24 25 26	23 33 33 43 54 75 75 75 75 75 75 75 75 75 75 75 75 75	, w w w w w w 4 w w v w v w v w v w v w v w v w v w v	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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R90951 standard; peptide; 7 AA.

RESULT R90951

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Factor VIII antigenic peptide corresp. to residues Glu1885-Phe1891. Factor VIII antigenic polypeptide fragments and epitope(s) - also inhibitors of factor VIII and anti-inhibitors, useful for e.g. preventing and treating immune disorders involving inhibition of factor VIII binding Factor VIII; modification; inhibitor activity; binding; antibody; von Willebrand factor; immune disorder. (CROI-) CROIX ROUGE BELGIQUE. 94BE-0000666. 95WO-BE00068 Laub R; 09-SEP-1996 (first entry) WPI; 1996-105861/11. Di Giambattista M, WO9602572-A2. 14-JUL-1995; 14-JUL-1994; 01-FEB-1996. Synthetic. 1 wyf

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Anti-microbial peptide; bee sting; melittin; haemolytic activity; bee venom; red blood cell; cell lysis; inhibition; Escherichia Coli; trypsin; D-amino acid; IC50.
                                                                                                                                                                                                                                                                     'note= "fluorenylmethoxycarbonyl-modified lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-melittin peptide(s) - useful for treating bee stings
                                                                                                                                                                                                                                                                                              /note= "D-form residue, C-terminal amide"
                                                                                                                                         Peptide #30 having anti-microbial activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Column 18; 26pp: English.
                                                                                                                                                                                                                                             Location/Qualifiers
                                                               W43253 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                         95US-0434761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houghten RA,
                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           (TORR-) TORREY PINES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-051545/05
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Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blondelle SE,
                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1995;
                                                                                                                 31-MAR-1998
                                                                                                                                                                                                                                                                                                                       US5698673-A
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                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                        W43253;
                                                    W43253
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         Peptides R90945-64 are derived from the factor VIII protein, esp. from a modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to von Willebrand factor, esp. antibodies, thus preventing or treating immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in R38104-21 represent protease-non-labile amino acid segments which may be substituted into the wild-type lipase protein of Humicola lanuginosa strain DSM 4106 at position 209-212 (see also R38101). The lipase resulting from these substitutions has improved stability against proteolytic degradation and is suitable for use in detergent compositions especially when used in conjunction with a protease.
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Protease-labile; lipase; Humicola lanuginosa; strain DSM 4106;
non-labile; stability; proteolytic degradation; detergent; protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein with improved stability against proteclytic degradation - comprises one or more protease labile aminoacid segments, substd. by non-labile segments used in detergents in conjunction with a
                                                                                                                                                                  ;
0
                                                                                                                                       Length 7;
                                                                                                                                                                  Indels
                                                                                                                                                                0
                                                                                                                                      100.0%; Score 43; DB 17;
100.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Svendsen A;
                                                                                                                                                                                                                                                                                                                                                         Protease-non-labile fragment #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 44; 55pp; English.
                                                                                                                                                                                                                                                                               R38120 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-DK00351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91WO-DK00350
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pathar SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-197071/24.
                                                                                                 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AA;
                                                                                                                                                                                        1 ETKSWYF 7
                                                                                                                                                                                                                etkswyf 7
                                                                                                                                                                                                                                                                                                                                 12-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                W09311254-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease
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                                                                                                                                                                                                                                                                                                        R38120;
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                                                                                                                                                                                                                                                       RESULT
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Pinilla C;

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Peptides represented by the formula (KFmoc)WYX, where X is any L-or D-amino acid and KFmoc is fluorenylmethoxycarbonyl-lysine, were synthesized and screened for anti-microbial activity against Escherichia coli. The present peptide showed anti-microbial activity with an IC50 value (concentration necessary to inhibit 50 per cent growth of bacteria) of 116 microg/ml. The invention provides peptides having anti-melittin activity with IC50 values of less than 30 microg/ml which are useful for treating melittin poisoning. Melittin is the active compound in bee yenom and causes cell lysis. Peptides having anti-melittin activity have one of the following formulae; Ac-IVILEZ-NH2; Ac-IVILEZ-NH2; Ac-IVINEZ-NH2; Ac-IVIQEPV-NH2; Ac-IVIQEPV-NH2; Ac-IVIQEPV-NH2; Ac-IVIQEPV-NH2; Ac-WIQIFI-NH2; where Z = an optionally methylated or chlorinated D-form or natural amino acid; Z1= F or I; Z2= I or Q; Z3= W or Y and Z4=C or F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.8%; Score 24; DB 19; Length 4; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W28886 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||
| wyf 4
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ID W2
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Gaps

0;

Indels

Length 4;

Query Match 55.8%; Score 24; DB 14; I Best Local Similarity 100.0%; Pred. No. 2.1e+05; Matches 3; Conservative 0; Mismatches 0;

WYF 7

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3

20-JAN-1998

W28886;

Synthetic

07-JUN-1995; 07-JUN-1995;

US5641861-A. 24 - JUN - 1997

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The peptide can be used in an oral care composition, comprising the peptide and an excipient. The peptide can be used to prevent or reduce bacteria adherence to teeth and/or coaggregation between plaque forming bacteria. It is useful for reducing or preventing periodontal disease, plaque, dental implant infection and dental caries when applied topically to tooth surfaces and/or tissues of the oral cavity. An effective dosage of the peptide is 0.02-0.1 g. Dimeric and cyclomonemeric anti-adherence peptides exhibit enhanced stability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a peptide with anti-adherence activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the acidic conditions and proteases which exist in the oral cavity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti adherence; oral care; dimer; cyclo monomer; polymer; plaque; periodontal disease; dental implant infection; dental carles; bacteria; teeth.
                                                                                                                                                                                           Anti adherence; oral care; dimer; cyclo monomer; polymer; plaque; periodontal disease; dental implant infection; dental caries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide(s) and their dimers, cyclo-monomer(s) and polymers useful for treating periodontal disease, plaque, dental implant infection and dental caries
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100.0%; Pred. No. 2.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-adherence peptide for use in oral care.
                                                                                                                                              Anti-adherence peptide for use in oral care.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murawaski SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 31; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  96GB-0011500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0466542.
W15206 standard; peptide; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charbonneau DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
                                                                                                                                                                                                                                          bacteria; teeth.
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995;
                                                                                         12-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1997.
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                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                               W15206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses the following new peptides, which are opioids which bind specifically to the mu receptor: Ac-Phe-Arg-Trp-Trp-Try-Xaa-NH2 (1);

Ac-Arg-Trp-Inc-G1y-Trp-Xaa-NH2 (2); Trp-Trp-Pro-Try-Trp-Trp-Trp-1(3);

Trp-Trp-Pro-Xaal-NH2 (4); Tyr-Pro-Phe-G1y-Phe-Xaa-NH2 (5);

Trp-Trp-Pro-Met-D-Trp-G1y-Xaa2-NH2 (6);

D-I1e-D-Met-D-Trp-Trp-G1y-Xaa2-NH2 (6);

D-I1e-D-Met-D-Trp-Trp-G1y-Xaa2-NH2 (7); Tyr-Al-B2-C3-NH2 (214);

Pm and red ((Me)X(H)y-Tyr-(NMe)z-Tyr-(Xaa3)z-NH2) (221); and

Trp-Trp-Pro-D4-(His)z-(Xaa)z-NH2 (222); Where Xaa = any natural amino

C Trp-Trp-Pro-D4-(His)z-(Xaa)z-NH2 (222); Where Xaa = any natural amino

acid; Xaal = Lys or Arg; n and z = 0 or 1; Xaa2 = G1y or the D form of

any naturally occurring amino acid; Al = D-norvaline or D-norleucine;

C any naturally occurring amino acid; Al = D-norvaline or D-norleucine;

C acid; Xaal = Lys or Arg; n and z = 0 or 1; Xaa2 = G1y or the D form of

any naturally occurring amino acid; Al = D-norvaline or D-norleucine;

C acid; Xaal = Lys or Arg; n and z = 0 or 1; Xaa2 = G1y or the D form of

any naturally occurring amino acid; Al = D-norvaline or D-norleucine;

C acid; Xaal = Lys or Arg; n and z = 0 or 1; Xaa2 = G1y or the D form of

assay and study of opiate receptor subtypes, particularly mu receptors

C in the Brain; (ii) for in vivo localisation of receptor subtypes; and

(iii) therapeutically to block the peripheral effects (e.g. constipation

c and prurtus) of centrally acting paln killers such as morphine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New opioid peptides which bind mu receptors specifically - have agonist or antagonist activity and are used for study and localisation of mu receptors and to treat peripheral side effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                         enkephalin; mu-opioid receptor ligand; agonist; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a specific example of peptide (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.8%; Score 24; DB 18; Length 6; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 /note= "the C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TORR-) TORREY PINES INST MOLECULAR STUDIES.
                                                                                                                                                                                                                                                                                    note= "N-acetyl-Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 8; 92pp; English
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ta and kappa receptor subtypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0487006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0487006
                                            (first entry)
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Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dooley CT, Houghten RA;
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                                                                                            Opioid peptide
                                                                                                                                                                                                                                                              Modified-site
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à g RESULT W15206

Sequence

Query Match

Ward SR;

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Gaps

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Length 6; Indels

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The present sequence represents a peptide with anti-adherence artivity. The peptide and be used in an oral care composition, comprising the peptide and an excipient. The peptide can be used to prevent or reduce bacteria adherence to teeth and/or coaggregation between plaque forming bacteria. It is useful for reducing or preventing periodontal disease, plaque, dental implant infection and dental caries when applied topically to tooth surfaces and/or tissues of the oral cavity. An effective dosage of the peptide is 0.02-0.1 g. Dimeric and processed the acidic conditions and proteases which exist in the oral cavity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a peptide with anti-adherence activity. The peptide can be used in an oral care composition, comprising the peptide and an excipient. The peptide can be used to prevent or reduce bacteria adherence to teeth and/or coaggregation between plaque forming bacteria. It is useful for reducing or preventing periodontal disease, plaque, dental implant infection and dental carries when applied topically to tooth surfaces and/or tissues of the oral cavity. An effective dosage of the peptide is 0.02-0.1 g. Dimeric and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti adherence; oral care; dimer; cyclo monomer; polymer; plaque; periodontal disease; dental implant infection; dental caries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating periodontal disease, plaque, dental implant infection and dental caries
                  useful for treating periodontal disease, plaque, dental implant
infection and dental caries
    New peptide(s) and their dimers, cyclo-monomer(s) and polymers
                                                                                                                                                                                                                                                                                                                                                                                                          Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SR;
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Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ward
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100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-adherence peptide for use in oral care.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charbonneau DL, Murawaski SL,
                                                                                Claim 1; Page 32; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 32; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W15209 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacteria; teeth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1997.
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1 wyf 3
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                                                                              96GB-0011500
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Matches 3; Conserv
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Sequence

Query Match

W15208;

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W15211 standard; peptide; 6 AA.
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cyclomonomeric anti-adherence peptides exhibit enhanced stability to the acidic conditions and proteases which exist in the oral cavity.
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                                                                                                                                DB 18; Length 6; 2.1e+05;
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                                                                                                                              55.8%; Score 24; DB 100.0%; Pred. No. 2.1 ive 0; Mismatches
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The peptide can be used in an oral care composition, comprising the peptide and an excipient. The peptide can be used to prevent or reduce bacteria anderence to teeth and/or coaggargation between plaque forming bacteria. It is useful for reducing or preventing periodoutal disease, plaque, dental implant infection and dental caries when applied topically to tooth surfaces and/or tissues of the oral cavity. An effective dosage of the peptide is 0.02-0.1 g. Dimeric and cyclomonomeric anti-adherence peptides exhibit enhanced stability to the acidic conditions and proteases which exist in the oral cavity.
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                                                           Anti adherence; oral care; dimer; cyclo monomer; polymer; plaque; periodontal disease; dental implant infection; dental caries;
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100.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 0;
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Anti-adherence peptide for use in oral care.
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The patent discloses eight new groups of opioid peptides which bind to the mu-receptor to act as agonists or antagonists. The peptides can be used for in-vitro assays to study opiate receptor subtypes (especially the mu type) in brain or other tissue samples; and for in-vivo diagnosis to localise opioid subtypes. The peptides are also useful as drugs to treat pathologies associated with other compounds which interact with the opioid receptor system. Therefore they can be used in medicaments for treating pathologies associated with the mu receptor and as analgesics. They can be used therapeutically to block the peripheral effects of centrally acting pain killers, e.g. 10 prevent side effects such as constipation and pruntitis associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leader sequence 50, development of substances against Bundyaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with morphine. The present sequence represents a specific example of one of the new groups of peptides, of formula Ac-Phe-Arg-Trp-Tyr-Xaa-NH2 where Xaa = a naturally occurring
                                                                                                                                                New mu opioid receptor binding ligand peptide(s) - useful for in-vitro and in-vivo diagnosis, as analgesics, and for blocking peripheral effects of centrally acting drugs, e.g. morphine
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                                     (TORR-) TORREY PINES INST MOLECULAR STUDIES.
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                                                                                                                                                                                                                          Disclosure; Page 17; 57pp; English.
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95US-0476438
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a peptide with anti-adherence activity. The peptide can be used in an oral care composition, comprising the peptide and an excipient. The peptide can be used to prevent or reduce bacteria adherence to teeth and/or coaggregation between plaque forming bacteria. It is useful for reducing or preventing periodontal disease, plaque, dental implant infection and dental caries when applied ropically to tooth surfaces and/or tissues of the oral cavity. An effective dosage of the peptide is 0.02-0.1 g. Dimeric and cyclomonearic anti-adherence peptides exhibit enhanced stability to the acidic conditions and proteases which exist in the oral cavity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "this residue is in C-terminal amide form"
                                                                                                                                                                                                                                                                                                    useful for treating periodontal disease, plaque, dental implant infection and dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt mu-receptor}; opioid; opiate; agonist; antagonist; diagnosis; analgesic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide which acts as mu-opioid receptor ligand.
                                                                                                                                                                                                                                           Ward SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Lot 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                       Murawaski SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-acetyl-Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.8%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 33; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R93744 standard; Protein; 6 AA.
                                                                                                                            96GB-0011500.
                                                                                                                                                                                                        (PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                   95US-0466542.
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                            03-JUN-1996;
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                                                    GB2307476-A
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                                                                                       28-MAY-1997
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                 Synthetic.
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Sequence

R93744;

RESULT 12

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Gaps

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5 WYF 7
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                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                         This is a peptide which is useful as a leader molecule. It is used for the development of substances active against enveloped pathogens such as viruses from the family Bundyaviridae. Its selection involved the reaction of a ligand library with the bound target pathogen and the pathogen bound ligands are subjected to competitive affinity-elution with at least one neutralising substance. The method is useful for comparative drug design to provide therapeutically active, protective and/or prophylactic substances and developing combinational therapies as well as for pathogen diagnostics. The method also identifies "leader molecules", which not only have great affinity, but also mimic the functions of known neutralising substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes opioid peptides, in which each of the N atoms in the peptide backbone between respective amino acids is modified by permethylation, perallylation, perethylation perbenzylation
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Opioid peptide; ligand binding; opioid receptor; micro-selective opioid peptide; enkephalin; opioid receptor system; blocking; peripheral effect; centrally acting pain killer; morphine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New opioid peptides useful for blocking the peripheral effects of centrally acting pain killers such as morphine
                                                                                                                                                                                                                                                                                                                                                                        ;
0
comparative drug design to provide therapeutically active, protective and prophylactic substances
                                                                                                                                                                                                                                                                                                                                   55.8%; Score 24; DB 19; Length 6; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Opioid peptide which inhibits binding of enkephalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TORR-) TORREY PINES INST MOLECULAR STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 8; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "amidated"
                                               Claim 16; Page 69; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y22992 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0488659
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghten RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-394647/33.
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                    6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5919897-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                      5 WYF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dooley CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y22992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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and pernaphthylation. The peptides inhibit ligand binding to an oploid receptor. Specifically, the peptides inhibit the micro-selective opioid peptide enkephalin. The peptides can be used in vivo diagnostically to localize opioid receptor subtypes. They can be used to treat pathologies associated with other compounds which interact with the opioid receptor system. The peptides are especially useful for blocking the peripheral effects of centrally acting pain killers such as morphine. Y22984-Y23003 represent optoid peptides of the invention, and are derived from the general sequence given in Y22983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is a peptide which is useful as a leader molecule. It is used for the development of substances active against enveloped pathogens such as viruses from the family Bundyaviridae. Its selection involved the reaction of a liquand library with the bound target pathogen and the pathogen bound ilgands are subjected to competitive affinity-elution with at least one neutralising substance. The meri of is useful for comparative drug design to provide therapeutically a protective and/or prophylactic substances and developing combinational theraptes as well as for pathogen diagnostics. The method also identifies a leader molecules, which not only have great affinity, but also mimic the functions of known neutralising substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leader sequence 51, development of substances against Bundyavirida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selection of target pathogen inhibiting substances - useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comparative drug design to provide therapeutically active, protective and prophylactic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%; Score 24; DB 20; L
ilarity 100.0%; Pred. No. 2.1e+05;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HELSINKI LICENSING LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W40932 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-F100339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-032807/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bundyaviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09745743-A1.
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Query Match 55.8%; Score 24; DB 19; Length 7; Best Local Similarity 100.0%; Pred. No. 2.1e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 5 WYF 7
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Qy 5 WYF 7 | 1 | Db 2 wyf 4 Search completed: January 17, 2001, 13:47:27 Job time: 266 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:44:46 Run on:

; Search time 13.66 Seconds
(without alignments)
34.795 Million cell updates/sec

US-08-765-837-7 43 1 ETKSWYF 7 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues Searched: 455 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:* Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	റ	alpha-dextrin endo	T-cell receptor be	receptor	dihydrofolate redu	locustakinin - mig	tryptophyllin, bas	ribulose-bisphosph	tubulin beta-3 cha	Ig heavy chain CRD		venom heptapeptide	glucose isomerase	FMRFamide-related	neuromodulatory pe	neuromodulatory pe	П	bradykinin-potenti		alcohol dehydrogen	dihydrofolate redu	T-cell receptor be	-cell receptor	T-cell receptor be	T-cell receptor be	c		T-cell receptor be	virotoxin ~ destro
SUMMARIES 3 ID	212	2 PN0649					2 A61081	Д					2 S17976					2 G37196							2 PT0726		2 PT0526	2 PT0642	1 A58725
Length DB	7 2	7	4															Ŋ											7
% Query Match L	41	41.9	34.9	34.9	34.9	34.9	34.9		ä	30.2	30.2		30.2				27.9		27.9	٠			ζ.	7.	۲.			27.9	27.9
Score	18	18	15	15	15	15	15	15	14	13	13	13	13	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12	12
Result No.	7	7	e	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23	24	25	26	27	28	29

.; 0

Caps ;

0; Indels

Ouery Match

41.9%; Score 18; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels

11: SWF 7 4 SWY 6

g à

RPCH-related neuro	T-cell receptor be	Cholecystokinin-5	20K protein - Rick	neuropeptide · sea	gut pentapeptide -	Ig heavy chain CRD	dnaA protein - Pse	cerebellar degener	T-cell receptor be	T-cell receptor be	T-cell receptor ga	hypothetical TCL3	triacylglycerol 11	hypothetical prote	major fat-globule
A34626	B53284	A32516	B31836	A60803	JH0253	PT0308	B34835	B35640	PT0629	PT0519	F41946	179564	S57274	S09652	B48394
0	~	7	~	7	7	7	7	~	7	7	7	4	7	7	7
4	41	Δ	ហ	S	S	2	9	9	9	9	9	9	7	7	7
9	، ب	۰	φ.	9.	9.	9.	७.	७.	9.	9	φ.	9.	9	9.	9.
25.6	25.6			25	25	25	25	25	25				25	25	25
11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
30	31	3.5	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

REBULT 1 S21230 dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment) C.Species: Phyllomedusa bicolor (two-colored leaf frog) C.Species: Phyllomedusa bicolor (two-colored leaf frog) C.Species: Phyllomedusa bicolor (two-colored leaf frog) C.Species: Saverini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Krell, FR Mignogna, G.; Severini, 1932 Lett. 302, 151-154, 1992 A; Fitle: Identification and characterization of two dermorphins from skin extracts of A; Reference number: S21152; MuID:92339502 A; Fatus: preliminary A; Recension: S21230 A; Status: preliminary A; Residues: 1-7 <mig. amino-terminal="" c.="" de<="" dermorphin="" homology="" precursor="" precursor;="" superfamily:="" th=""></mig.>

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tryptophyllin, basic - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Accession: A61081
R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
Int. J. Pept. Protein Res. 33, 391-395, 1989
A;Title: Isolation, structure determination and synthesis of a novel tryptophan-conta A;Reference number: A61081
A;Mocession: A61081
A;Mocession: A61081
A;Mocession: A61081
C;Comment: The blological activity of this peptide was not determined.
C;Comment: The blological activity of this peptides
C;Comment: The blological activity of this peptides
C;Comment: amidated carboxyl end; hydroxyproline; skin
F;3/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (f C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
C;Accession: Pr0087
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
Submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and standardization A;Reference number: PN0173
                                                                                                                                                                                                                                                                                           C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C;Accession: A61068
E;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A. Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, A;Reference number: A61068; MUID:92262851
A;Reference number: A61068
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                                                Gaps
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A;Mosaidues: 1-6 <SCH>
C;Keywords: anidated carboxyl end; cephalomyotropic peptide; neuropeptide
F;6/Modified site: amidated carboxyl end (Gly) #status experimental
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Pred. No. 2e+05;
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100.0%; Pred. No. 2e+05;
tive 0; Mismatches 0;
          100.0%; Preu. ....
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                    Best Local Similarity 100.
Matches 2; Conservative
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                                                                                                                                                                                                              J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601
A;Accession: PT0580
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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                                                                                            T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
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.larity 100.0%; Pred. No. 2e+05;
Conservative 0; Mismatches 0; Indels
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A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: day 19 fetal thymus, strain BALB/c C;Keywords: T-cell receptor
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A; Status: translation not shown
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Best Local Similarity
Matches 2; Conserv
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A; Residues: 1-5 <FEE>
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Cydrosesion: 317976
R.Lee, C.; Zeikus, J. G.
Biochem J. 273, 565-571, 1991
A;Title: Purification and characterization of thermostable glucose isomerase from Clo A;Reference number: S15119; MUID:91144536
A;Recession: S17976
A;Status: preliminary
A;Molecule type: protein
A;Rote transpector of the sequence from page 568 is inconsistent with that from page 565 in having A;Note: the source is designated as Thermoanaerobacter strain B6A
                            Theavy chain CRD3 region (clone 4-91C) - human (fragment)
C; Species: Homo sapiens (man)
C; S
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C;Species: Conus imperials (imperial cone)
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 07-May-1979
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 07-May-1979
C;Accession: A58512
B;Craig, A.G.; Jimenez, E.C.; Dykert, J.; Nielsen, D.B.; Gulyas, J.; Abogadie, F.C.; J. Biol. Chem. 272, 4689-4698, 1997
A;Title: A novel post-translational modification involving bromination of tryptophan. A;Reference number: A58512; MuID:97184108
A;Accession: A58512
A;Molecule type: protein
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C;Species: Thermoanaerobacterium saccharolyticum
C;Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 17-Apr-1998
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C; Superfamily: unassigned conotoxins
C; Superfamily: unassigned conotoxins
C; Superfamic acid; venom
F; J, Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; F, Modified site: 6-bromotryptophan (Trp) #status experimental
F; 7/Modified site: amidated carboxyl end (Cys) #status experimental
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Pred. No. 2e+05;
2; Mismatches
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Pred. No. 2e+05;
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Best Local Similarity 33.3%;
Matches 1; Conservative
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ilarity 33.3%;
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Best Local Similarity
Matches 1; Conserv
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Development 116, 543-554, 1992
A;Title: Ultrabithorax is a regulator of beta-3 tubulin expression in the Drosophila vis A;Reference number: S33567; WUID:93170162
A;Accession: S33567
A;Accession: S33567
A;Status: preliminary; translation not shown
A;Molecule type: DNA
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C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: PT0278
R; Yamada, M: Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
J. Exp. Med. 173, 395-407, 1991
A; Reference number: PT0222; MUID: 91108337
A; Reference number: PT0222; MUID: 91108337
A; Residues: 1-5 <VAM>A; Residues: heterotetramer; hmmunoglobulin
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
C;Accession: S33567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)
A;Molecule type: protein
A;Residues: 1-7 <TSU>
A;Experimental source: leaf
C;Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase
F;1/Modified site: acetylated amino end (Ser) #status experimental
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0; Indels
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2e+05;
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Pred. No.
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A;Cross-references: FlyBase:FBgn0003888
A;Introns: 5/3
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Matches 2; Conserv
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Best Local Similarity
Matches 3; Conserv
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FWRFamide-related heptapeptide - Panagrellus redivivus C;Species: Panagrellus redivivus C;Species: Panagrellus redivivus C;Species: O3-May-1994 #sequence_revision 15-oct-1994 #text_change 11-Jul-1997 C;Accession: PC2132 R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, T.G.; Thim, Biochem Biophys. Res. Commun. 200, 973-980, 1994 A;Title: KGAYWRFamide: a novel FMRFamide-related heptapeptide from the free-living nematary. PC2132; MUID:94235053
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R. Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
R. Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
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C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
                                                                                                           Gaps
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A.Molecule type: protein
A.Residues: 1-7 - AMAU>
C.Keywords: amidated carboxyl end
F.7/Modified site: amidated carboxyl end
Query Match 30.2%; Score 13; DB 2; Length 7; Best Local Similarity 100.0\%; Pred. No. 2e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:47:31; Search time 8.41 Seconds (without alignments) 26.880 Million cell updates/sec Run on:

US-08-765-837-7 43 1 ETKSWYF 7

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 seqs, 32294092 residues Searched:

72 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITMMADIFC

	Description	locus	m	P41874 panagrellus		P35921 achatina fu	P30425 bothrops in					P06294 dactylium d	~		P82158 cydia pomon			P31890 ascaris suu		P42563 hirudo medi	P81817 carcinus ma	P41853 artioposthi	P01373 periplaneta		P81806 carcinus ma	P81807 carcinus ma	_	P42564 hirudo medi	P99025 mus musculu	3	984	81675	5904	P19918 pseudomonas
SUMMARIES	ID	LOK1_LOCMI	FAR3_HAECO	FAR3_PANRE	WWA1_ACHFU	WWA3_ACHFU	BPP7_BOTIN	UF01_MOUSE	WWA2_ACHFU	TUFT_HUMAN	PAP2_PARMA	IGAO_DACDE	UC22_MAIZE	FARP_MONEX	ALL7_CYDPO	UC24_MAIZE	ALL2_CARMA	FAR2_ASCSU	FAR3_HIRME	FAR4_HIRME	AL14_CARMA	FARP_ARTTR	PRCT_PERAM	OVM_LEPDE	ALL3_CARMA	ALL4_CARMA	ALL5_CARMA	FAR5_HIRME	GFRP_MOUSE	HY7_PIG	MNP1_LEPDE	UNO6_PINPS	ACH1_ACHFU	DCMS_PSECH
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P4256) hirudo medi P01162 macrocallis P19931 achicta dome P54714 canis famil P13973 escherichia P13736 mytilus edu P13737 mytilus edu P23210 herpes simp P2310 herpes simp P21832 enterococcu P11832 enterococcu P31889 ascoris suu P41871 helisoma tr
FLRE HIRME FMRE_MACNI SUGA_ACNDO SUGA_ACNEA TRM3_ECOLI CIPL_MYTED CIPL_MYTED VP19_HSV1K CCF1_ENTFA CCF1_ENTFA FAR1_ASCSU
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ALIGNMENTS

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LOCMI STANDARD; PRT; 6 AA. 1: 1v-1995 (Rel. 32, Created) 1v-1995 (Rel. 32, Last sequence update) 1v-1998 (Rel. 36, Last annotation update) 1r-1998 (Rel. 36	Pterygota: Neoptera: Orthopteroldea: Orthoptera; Caellfera; Acridomorpha; Acridoidea; Acrididae; Locusta. [1] [1] [1] [2] [2] [3] [4] [4] [5] [5] [6] [7] [7] [7] [7] [7] [7] [7] [7] [7] [7	OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN TUBULES. A61068; A61068. A61068 A61068. RES 6 6 6 6 6 6 6 ENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64; ENCE 6 AA; 654 WW; 686365A5B9CDB000 CRC64; atch 34.9%; Score 15; DB 1; Length 6; cal Similarity 100.0%; Pred. No. 8.9e+04; 2; Conservative 0; Mismatches 0; Indels 0; Gaps	4 SW 5 1 1 4 SW 5 1 1 4 SW 5 1 1 2 EAR3. HAECO STANDARD; PRT; 7 AA. PB1298. 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update) FWRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMRF-AMIDE). FWRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMRF-AMIDE). FULL SCOUTE STATE
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ID BPP7_BOTIN
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                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                 SEQUENCE, AND SYNTHESIS.
MADLINE-94235053; PubMed-8179635;
Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
Geary T.G., Thim L.;
"KRAYMFRamide a novel FMRFamide-related heptapeptide from the free-
living nematode, Panagrellus redivivus, which is myoactive in the
parasitic nematode, Ascarls suum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; "WMamide-1, -2 and -3: novel neuromodulatory peptides isolated from
                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 200:973-980(1994).
-!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT MUSCLE TENSION INCREASE.
-i- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
-i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                                 Score 13; DB 1; Length 7;
Pred. No. 8.9e+04;
); Mismatches 1; Indels
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Pred. No. 8.9e+04;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
                                         AMIDATION.
69D4068B5DC5B350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION.
69D4068B5DC5B350 CRC64;
                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last Sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMRF-AMIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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MEDLINE-93265912; PubMed-8495720;
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ilarity 75.0%;
Conservative
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75.0%;
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MOD_RES 7 7 7
SEQUENCE 7 AA; 902 MW.
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                                Neuropeptide; Amidation.
                                                                                                                                                                                                     STANDARD;
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                                                                        Query Match
Best Local Similarity
The 3; Conserve
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P35919;
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SEQUENCE
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Best Local S
Matches 3
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FAR3_PANRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
-!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
PIR; 533245; 533245.
Neuropeptide; Amidation.
MOD_RES
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica."; FEBS Lett. 323:104-108(1993).
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1-FBE-1994 (Rel. 28, Last sequence update)
01-FBE-1994 (Rel. 28, Last annotation update)
BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bothrops insularis (Island jararaca) (Queimada jararaca).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
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                                                                                                                                                                                                                       30.2%; Score 13; DB 1; Length 7;
40.0%; Pred. No. 8.9e+04;
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7 AA; 993 MW; 7362D5B69B041310 CRC64;
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40.0%; Pred. No. 8.9e+04;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WMAAL ACHFU STANDARD; PRT; 7 AA. P35921; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) WMAMIDE-3.
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TISSUE-GANGLION;
MEDLINE-93265912; PubMed-8495720;
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MEDLINE=90351557; PubMed=2386615;
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                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.00.
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Best Local Similarity
...... 2; Conserv?
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Fidalgo B.V., Najjar V.A.;

The physiological role of the lymphoid system. VI. The stimulatory effect of laucophilic gamma globulin (Leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.;

Biochemistry 6:3386-3392(1967).

Hischlamstry 6:3386-3392(1967).

CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN. TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
PARDAXIN II (PXII) (FRAGMENT).
Pardachium marmoratus (Red sea moses sole).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euceleostom!; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Solecidei; Soleidae; Pardachirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Blophys. Res. Commun. 47:172-179(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           Indels
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                                                                                                                                                   Length 7;
                                   AMIDATION.
7362D5B686D32310 CRC64;
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                                                                                                                                                Score 11; DB 1; L4 Pred. No. 8.9e+04;
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                                                                                                                               25.6%; Sco. 100.0%; Pred. No. 0. 0. 0. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AA.
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21-JUL-1986 (Rel. 01, Last seq
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PIR; A02147; A02147.
MIM; 191150; ...
SEQUENCE 4 AA: 501 ...
                                                              7 AA; 964 MW;
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  Neuropeptide; Amidation. MOD_RES 7 7
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                                                                                                                      Query Match
Best Local Similarity
Thes 1; Conserve
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Best Local Similarity
Matches 2; Conserv
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ID TUFT_HUMAN
AC P01858;
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P81864;
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Achatinacea; Achatinidae; Achatina.
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"Wmanide-1." 2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95009907; Pubmed-7523108; MEDLINE-95009907; Pubmed-7523108; Merzick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; Merzick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis."; Electrophoresis 15:735-745(1994).

-I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROPEIN IS: 6.6, ITS MW IS: 19 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
J. Protein Chem. 9:221-227(1990).
-!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT. IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
PIR; G37196; G37196.
                                                                                                                                                                                                   5 AA; 629 MW; 776DC37326B00000 CRC64;
                                                                                                                                                                                                                                                                                                                   Score 12; DB 1; Length 5;
Pred. No. 8.9e+04;
1; Mismatches 1; Indels
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Last annotation update)
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MEDLINE-93265912; PubMed-8495720;
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01-JUN-1994 (Rel. 29, Last seq
01-OCT-1994 (Rel. 30, Last anno
                                                                                                                                                                                                                                                                                                                      27.9%;
                                                                                                                                                                           Hypotensive agent; Venom. MOD_RES 1
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Best Local Similarity
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Best Local Similarity
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P38639;
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Touvet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
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"GNFFRFamide: a novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm, Moniezia expansa.";
Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
-i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYDIASTATIN 7.
CYDIASTATIN 7.
Evalua pomonella (Codling moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moniezia expansa (Sheep tapeworm).
Eukaryota; Metazoa; Platyhelminthes; Neodermata; Cestoda; Eucestoda;
Cyclophyllidea; Anoplocephalidae; Moniezia.
                                                                                 genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-I- MISCELLANEOUS. ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIL IS: 6.1, ITS MW IS: 30.4 KDA.
MAIZE-ZDPAGE: P80628; COLEOPTILE.
                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                5 AA; 654 MW; 72CB19C9C0300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION. * 69D409C9C4481000 CRC64;
                                                                                                                                                                                                                                         DB 1; Le . 8.9e+04;
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Pred. No.
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50.0%;
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Best Local Similarity
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Best Local Similarity
                              TISSUE-COLEOPTILE;
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P82158;
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FARP_MONEX
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ALL7_CYDPO
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           TISSUE=SKIN SECRETION;
MEDLINE=87057369; PubMed=3782138;
Lazarrovici P., Primor N., Loew L.M.;
Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea moses sole (Pardachirus marmoratus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fed. Proc. 31:447-447(1972).
-1- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY BINDING TO ITS PROSTHETIC COPPER GROUP.
PIR; A01341; XEYDGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                Gaps
                                                                                           J. BLOI. Chem. 261:16704-16713(1986).
-1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
-1- SUBUNIT: MONOMER. IN AQUEDOUS SOLUTION EXISTS AS A TETRAMER.
-1- SUBCELLULAR LOCATION: SECRETED.
-1- SIMILARITY: BELONGS TO THE PARBAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; 2ea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avigad G., Markus 2.;
"Identification of a peptide inhibitor of galactose oxidase from
Dactylium dendroides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 474)
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Pred. No. 8.9e+04;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                         7769C9C9C8100000 CRC64;
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SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
GALACTOSE OXIDASE INHIBITOR.
Dactylium dendroides (Cladobotryum dendroides).
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TOUZET P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
The maize two dimensional gel protein database: towards an integrated
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.0, ITS MW IS: 30.0 KDA.
MAIZE-2DPAGE; P80630; COLEOPTILE.
MAIZEDB; 123956; -.
NON_TER 1 1
SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
                                                                                                 Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
MOD RES
7 AMIDATION.
SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.9%; Score 9; DB 1; Length 7; 40.0%; Pred. No. 8.9e+04; tive 1; Mismatches 2; Indels
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                                 TISSUE=LARVA;
MEDLINE-98054539; PubMed-9392829;
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Best Local Similarity 40.05
Matches 2; Conservative
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DT 01-OCT-1996
DF 15-JUL-1999
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09/199 human adeno P82101 litoria rub P82099 litoria rub P82100 litoria rub

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P72081 Q47508 Q47477 Q28742 P92421 P92385 J

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TISSUE-SKIN SECRETION:
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyber M.J., Wallace J.C.;
Tyber M.J., Wallace J.C.;
The structure of new peptides from the Australin red tree froq
Litoria rubella'. The skin peptide profile as a probe for the
Litoria rubella'. The skin peptide profile as a probe for the
cevolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
I- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTRASMITTER.
I- FUNCTION: MAY ACT AS NEUROMODULATOR OR NEUROTRASMITTER.
I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
I- MASS SPECIFICITY: MW-965; METHOL-FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 13; Length 7; Pred. No. 3.7e+05; 1; Mismatches 0; Indels
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     983 MW;
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NCBI_TaxID=104895;
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P82541 spinacia ol
P82096 litoria rub
045245 saccharomyc
04923 glycine max
P82182 spinacia ol
P82182 spinacia ol
047029 enterobacte
P82070 litoria rub
P82070 litoria rub
P82073 litoria rub
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

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score greater than or equal to
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6 AA.

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PRELIMINARY;

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Laux T., Goldberg R.B.;
"A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (Soybean).
Bukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                       Mitochondrion.
Eukaryota; Fungi, Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                           MEDLINE-81069885; PubMed-6254986; Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino C "Assembly of the mitochondrial membrane system. Structure and nucleotide sequence of the gene coding for subunit 1 of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.6%; Score 11; DB 10; Length 7; Best Local Similarity 100.0%; Pred. No. 3.7e+05; Matches 1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HMG-1-LIKE PROTEIN (FRAGMENT).
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NON_TER
1 1 1 SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;
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                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 19:4769-4769(1991).
                                                                                                                                                                                                                                                                                                                                                   255:11927-11941(1980).
                                     PRT;
                                                                                                                                                                                           Saccharomycetaceae; Saccharomyces.
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STRAIN-CV. ESSEX; TISSUE-ROOTS;
MEDLINE-91367679; PubMed=1891369;
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J. Biol. Chem. 255:11927-119
EMBL; V00694; CAA24066.1; -.
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                                                                                  Chloroplast.
Sukaryota: Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                        Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 BETA (FRAGMENT).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AA; 732 MW; 63333735A411C000 CRC64;
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6 AA; 792 MW; 6683704772C9A000 CRC64;
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Pred. No. 3.7e+05;
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Aust. J. Chem. 52:0-0(1999).
                                                                  Spinacia oleracea (Spinach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.; "Analysis of the aac(3)-VIa gene encoding a novel 3-N-acetyltransferase."; Antimicrob. Agents Chemother. 37:2074-2079(1993).

EMBL. M88012: AAA16193.1; -1.

SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylldae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 1.1.
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675 MW; 6321B415B05DB000 CRC64;
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                                                                      DB 10; L
3.7e+05;
                                                                      23.3%; Score 10; DB 100.0%; Pred. No. 3.7 Live 0; Mismatches
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
AAD Al PROTEIN (FRAGMENT).
                                                                         Query Match 23.3
Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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  6 AA;
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P82070;
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last amontation update)
01-JUN-2000 (TrEMBLrel. 14, Last amontation update)
CHLOROPLAST 50S **RBOSOMAL PROTEIN LIO BETA (FRAGMENT).
Spinacia oleracea (Spinach).
Bukaryota: viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicocytedons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
NCBL_TaxID-3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. ALWARO; TISSUE-LEAF;
Yamaguchi K., von Knoblauch K., Subramanian A.R.;
Yamaguchi K., von Knoblauch K., Subramanian A.R.;
Identification of all the proteins in the large subunit of an organelle (chloroplast) ribosome.";
J. Biol. Chem. 0:0-0(2000).
I. Biol. Chem. 0:0-0(2000).
I. SINILARION: THIS PROFEIN BINDS DIRECTLY TO 23S RIBOSOWAL RNA.
II SSUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
II TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
II SIMILARIYY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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P82182;
01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CHLOROPLAST 50S RIBOSOWAL PROTEIN L10 GAMMA (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein; Chloroplast; rRNA-binding.
                                                                                                                                                                          6 AA.
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Best Local Similarity
Matches 2; Conserv
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Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY
               ANTIBIOTIC ACTIVITY.
--- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
---- MASS SPECIFORTRY: MW-655; METHOD-FAB.
Amphibian skin; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-COOPER;

BDLINE=95313343; PubMed=7793062;
Vlcek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.
Letchworth G.J., Schwyzer M.;
                                                                                                                                                                             Indels
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                                                                                                                                               Length 5;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN (FRAGMENT).
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                                                                              5 AMIDATION.
5 AA; 656 MW; 71A9C9CB10300000 CRC64;
                                                                                                                                             20.9%; Score 9; DB 13; 50.0%; Pred. No. 3.7e+05;
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                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 1; Conserv
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Aust. J. Chem. 49:955-963(1996).

-I. FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 3.1.
Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the sof evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND MASS SPECTROMETRY.
TISSUE-SKIN SECRETION:
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
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-i- MASS SPECTROMETRY: MW=626; METHOD=FAB.
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                                 DB 13; Leus, 3.7e+05;
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6DD9C9CAB2A00000 CRC64;
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Pred. No. 3.7e-
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ilarity 50.0%;
Conservative
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AA;
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Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs
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MEDLINE=96427318; PubMed=8830682;
Rehm B.H.A., Etresvag H., Valla S.;
Rehm B.H.A., Etresvag H., Valla S.;
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5899(1996).
EMBL; X87973; CAA61230.1;
"Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a colinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus.";

EMBL: Z48053; CAA88130.1; --
Hypothetical protein.

NON TER

SEQUENCE 7 AA; 758 MW; 6DD33455BIFIBICO CRC64;
                                                                                                                                                                                                                                                                                                                       Gaps
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(Haemophilus actinomycetemcomitans).
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER 1 1
SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AEDO CRC64;
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STRAIN-ATCC 33384;
MEDLINE-96355846; Pubmed-8751884;
                                                                                                                                                                                                                                                              Query Match 18.6%;
Best Local Similarity 66.7%;
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azotobacter vinelandii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=354;
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DT 01-JUN-
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GN GLYA.
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Kraig E.;
"cis Blements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus actinomycetemcomitans.";
Infect. Immun. 64:3451-3460(1996).
EMBL: US1862; AAB88721.1;
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                                                                                                                                                                                                SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
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Job time: 106 sec
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Sequence 2, M Sequence 6, M Sequence 12, Sequence 12, Sequence 2, M Sequence 6, M Sequence 6, M

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Sequence 2, A Sequence 6, A Sequence 4, A Sequence 26, A Sequence 26,

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
US-08-321-625-28
US-08-321-625-29
US-08-321-625-76
US-08-487-006-94
US-08-433-318A-2
US-08-467-607-12
US-08-469-362-12
US-08-922-048-2
US-08-922-048-2
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US-08-321-625-70
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                                                                                                                                                                                                                                           US-08-321-625-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 4600-032.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 323-8302
TELEPRA: (415) 323-8306
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: YEACHININ RELEASE #1.0, VEES
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/653,091A
FILING DATE: U8-FEB-1991
CLASSIFICATION ATA:
APPLICATION NUMBER: US 07/366,313
FILING DATE: 13-JUN-1989
FRICK APPLICATION DATA:
FILING DATE: 13-JUN-1989
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 06/948,270
FILING DATE: 31-DEC-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/07653091A
Patent No. 5614366
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.,
APPLICANT: Hadlock, Kenneth G.
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JURESS:
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANIAN
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     77000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: HTLV-II
US-07-653-091A-8
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US-07-653-091A-8
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     Sequence 8, Appli
Sequence 112, Appli
Sequence 113, Appli
Sequence 114, Appli
Sequence 115, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 6, Appli
Sequence 108, Appli
Sequence 170, Appli
                                                                                                                                       (without alignments)
10.492 Million cell updates/sec
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                                                                                                                       ; Search time 11.98 Seconds
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Sequence 8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
                   GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08-488-659A-108
-08-996-338-15
-08-665-220-70
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US-08-481-598-8

US-08-483-353-8

US-08-483-353-8

US-08-014-979-113

US-08-014-979-113

US-08-014-979-113

US-08-014-979-114

US-08-014-979-114

US-08-08-487-006-16

US-08-487-006-16

US-08-487-006-108

US-08-487-006-108

US-08-488-659A-15

US-08-996-338-15

US-08-996-338-15

US-08-996-338-15

US-08-996-338-15

US-08-996-338-15

US-08-996-338-15

US-08-996-338-15

US-08-996-338-15

US-08-991-122-39

US-08-991-122-37
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                                                                                                                                                                                                                                                                                                             174772 seqs, 17957048 residues
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                                                                                                                     January 17, 2001, 13:43:41
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                         1 ETKSWYF 7
                                   Copyright
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                                                                                                                                                                                                         Perfect score:
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                                                                                     OM protein
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HTLV-II Peptide Antigens and

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RESULT 3
US-08-481-598-8
; Sequence 8, Application US/08481598
; Patent No. 581441
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
TITLE OF INVENTION: HTLV-I AND HTLV-II Peptide Antigens and TITLE OF INVENTION: Methods
; TORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc., Legal Dept.
; STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.1%; Score 25; DB 2; Length 6; 75.0%; Pred. No. 1.3e+05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,598
FILING DATE: 07 -JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/653,091
FILING DATE: 08-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,313
FILING DATE: 13-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 306/948,270
FILING DATE: 31-DEC-1986
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, Allan A.
RESTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/COMMINICATION INFORMATION:
TELEPHONE: (415) 368-0709
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGEL = mnin arid
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US-08-483-353-8
Sequence 8, Application US/08483353
Patent No. 5871933
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HTLV-II
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Best Local Similarity
Matches 3; Conserv
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Patent No. 5763572
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Hadlock, Kenneth G.
TITLE OF INVENTION: HTLV-I AND HTLV-II Peptide Antigens and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc., Legal Dept.
STREET: 505 Penobscot Drive
CITY: Redwood City
CETT: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 1; Length 6;
Pred. No. 1.3e+05;
1; Mismatches 0; Indels
                                                                               Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,068
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/653,091
FILING DATE: 08-FEB-1991
PRIOR APPLICATION NUMBER: US 07/366,313
APPLICATION NUMBER: US 07/366,313
FILING DATE: 13-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/948,270
FILING DATE: 31-DEC-1986
ATTORNEY/AGENT INFORMATION:
                                                                           Score 25; DB 1; Le
Pred. No. 1.3e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, Allan A.
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: G4C1P2D1
TELECOMNUNICATION INFORMATION:
TELEPHONE: (415) 369-9500
TELEPRA: (415) 368-0709
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                           58.1%;
ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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FRAGMENT TYPE: intern
ORIGINAL SOURCE:
ORGANISM: HTLV-II
US-08-485-068-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                           Query Match
Best Local Similarity
Matches 3; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
                                                                                                                                                           4 SWYF 7
                                                                                                                                                                                                   2 SWYY 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SWYF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                            US-08-485-068-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watches
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Gaps

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US-08-014-979-112

Sequence 112, Application US/08014979

Sequence 112, Application US/08014979

Patent No. 5510240

GENERAL INFORMATION:

APPLICANT: Lam, Kit S. et al.

TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof;

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 2; Length 6;
Pred. No. 1.3e+05;
1; Mismatches 0; Indels
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                                                                                                              MEDIUM TIPE: FLORPY GISK
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,702
FLING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/653,091
FILING DATE: 08-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,313
FILING DATE: 13-JUN-1989
PRIOR APPLICATION WARA:
APPLICATION NUMBER: US 07/366,313
FILING DATE: 31-DEC-1986
ATTORNEY/AGENT INFORMATION:
ANDELSON TO NUMBER: US 06/948,270
FILING DATE: 31-DEC-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G4C1P2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, Allan A.
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: G4C11
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 369-9500
TELEPAX: (415) 368-0709
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.18;
75.08;
                                                                                                                                                                                                                                                                Floppy disk
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 6 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-CONTROLL NO 
                                                                                                                                                                                      ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                  Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HTLV-II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SWYF 7
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-473-702-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
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Patent No. 5928861
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hadlock, Kenneth G.
TITLE OF INVENTION: HTLV-I AND HTLV-II Peptide Antigens and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc., Legal Dept.
...r.LCANT: Hadlock, Kenneth G.
TITLE OF INVENTION: HTLV-I AND HTLV-II Peptide Antigens and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.1%; Score 25; DB 2; Length 6; 75.0%; Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRESASE #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,353
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/653,091
FILING DATE: 08-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/948,270
FILING DATE: 13-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/948,270
FILING DATE: 31-DEC-1986
ATTORNEY/AGENT INFORMATION:
NAME: BEOOKES: Allan A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/FOCKET NUMBER: 36,373
REFERENCE/FOCKET NUMBER: 36,373
REFERENCE/FOCKET NUMBER: 36,373
TELEPHONE: (415) 369-9500
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                     STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: HTLV-II
US-08-483-353-8
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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STATE:
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CURRENT APPLICATION DATA: US/08/014,979
                                      APPLICATION NUMBER: US/08/014
FILIME DATE: 19930208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 7156
REFERENCE/DOCKET NUMBER: 7156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPHONE: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /label= F
OTHER INFORMATION: /note= "l:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18,872
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TELECOMMUNICATION: 212 790-9090
TELEFRAX: 212 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site LOCATION: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
--hes 3; Conservative
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
COTHER INFORMATION:
US-08-014-979-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 WYF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= F
/note= "linked with ONb (an organic molecule)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 113, Application US/08014979
Patent No. 5510240
GENERAL INFORMATION:
APPLICANT: Lam, Kit S. et al.
TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof UNDER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- W /note= "9-fluorenylmethoxycarbonyl (Fmoc) bound "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Xaa
/note= "Xaa is beta-Ala-ACA-EDA-PepSyn K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.8%; Score 24; DB 1; Length 4; 100.0%; Pred. No. 1.3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: 0.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SGFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "(0-t-Bu) bound"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,979
FILING DATE: 19930208
CLASSIFICATION: 435
                                                                                                                                                                 7156-041
                                                                                                                 NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYRE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
LOCATION: 2
INCREINSORMATION: /label- Y
OTHER INFORMATION: /note-"(C
                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
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NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: Î:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 4

CTHER INFORMATION:
CTHER INFORMATION:
US-08-014-979-112
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-014-979-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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Gaps
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Sequence 114, Application US/08014979

Sequence 114, Application US/08014979

GENERAL INFORMATION:

APPLICANT: Lam, Kit S. et al.

TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof;

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
/note= "linked with ONb (an organic molecule)"
                                                                                               /label- xaa
/note= "xaa is beta-Ala-ACA-EDA-PepSyn K"
                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                          55.8%; Score 24; DB 1; Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19930208
CLASSIFICATION: 435
                                                                                                                                                                                                                                                 100.0%; Pred. No. 1.3e+05; ive 0; Mismatches 0;
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LOCATION: 3
OTHER INFORMATION: /label- F
OTHER INFORMATION: /note- "linked with ONb (an organic molecule)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861el Mu Opioid Receptor Ligands: TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amino acid is acetylated at the N-terminal."
                                                                                                                                                                                                                                                                                                                                                                                                                                   55.8%; Score 24; DB 1; Length 4; 100.0%; Pred. No. 1.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: Modified-site
COCATION: 4
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "-beta-Ala-ACA-4-MBHA"
US-08-014-979-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
LENTH: 6 anno acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08487006
Patent No. 5641861
GENERAL INFORMATION:
                                                                                                                                                                       NAME/KEY: Modified-site LOCATION: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.8%
Best Local Similarity 100.0
Matches 3; Conservative
                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-487-006-16
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| WYF 3
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/note- "linked with OND (an organic molecule)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lam, Kit S. et al.
TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof
CORRESPONDENCES: 12.
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.8%; Score 24; DB 1; Length 4; ilarity 100.0%; Pred. No. 1.3e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Xaa
/note= "-beta-Ala-ACA-4-MBHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= Y
OTHER INFORMATION: /note= "(O-t-Bu) bound"
FEATURE:
                                                                                                                                                                                           NAME/KEY: Modified-site
LOCATION: 1
LOCATION: 1
LOCAMEN OF A Label W
OTHER INFORMATION: /note= "Fmoc bound"
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FILING DATE: 19930208
CLASSIFICATION: 435
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Sequence 115, Application US/08014979
Patent No. 5510240
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INPORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7156
TELECOMMUNICATION INFORMATION:
TELEFAN: 212 790-9090
TELEFAX: 66141 PENNIE
                          114:
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
TELEX: 6614 PENNIE
INFORMATION FOR ESQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 3
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-014-979-114
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Best Local Similarity
Matches 3; Conserv
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1 WYF 3
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Gaps
                                                                        Sequence 6, Application US/09260190

Sequence 6, Application US/09260190

Patent No. 6096713

GENERAL INFORMATION:

APPLICANT: Green, Lawrence R.

TITLE OF INVENTION: Pharmaceutical Angiostatic Dipeptide

TITLE OF INVENTION: Compositions and Methods of Use Thereof

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
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Patent No. 6056713
Patent No. 6056713
Patent No. 6056713
Papticant: Green, Lawrence R. APPLICANT: Blasecki, John W. TITLE OF INVENTION: Compositions and Methods of Use Thereot NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 3; I
Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/260,190
FILING DATE: 01-MAR-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/538,701
FILING DATE: 03-CCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,764
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Powers, Margaret A.
REGISTRATION UNBABER: 39,804
REFERENCE/DOCKET NUMBER: 0155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-260-190-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                      US-09-260-190-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-260-190-4
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                                                                                                                                55.8%; Score 24; DB 1; Length 6; llarity 100.0%; Pred. No. 1.3e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.8%; Score 24; DB 2; Length 6; 100.0%; Pred. No. 1.3e+05; Live 0; Mismatches 0; Indels
                       /note= "Amino acid is amidated at
the C-terminal."
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the C-terminal."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,659A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08488659A
Patent No. 5919897
GENERAL INFORMATION:
APPLICANT: Booley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPOMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDRER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1705
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 6 amino acids TYPE: amino acid
; LOCATION: 6
; CTHER INFORMATION:
; CTHER INFORMATION:
US-08-487-006-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
COTHER INFORMATION:
US-08-488-659A-16
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                  /note= "All amino acids are D-amino acids."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acid is amidated at
the C-terminal."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell and Flores ' 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: Mu Optoid Receptor Ligands:
TITLE OF INVENTION: Mu Optoid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.5%; Score 23; DB 1; 175.0%; Pred. No. 1.3e+05; iive 1; Mismatches 0
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TYPE: amino acid
FATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/488,659A FILING DATE: 07-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108, Application US/08488659A Patent No. 5919897 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: , OTHER INFORMATION: & FEATURE: NAME/KEY: PEPLIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
COTHER INFORMATION:
US-08-487-006-108
                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-488-659A-108
                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Patent No. 5641861
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861e1 Mu Opioid Receptor Ligands:
TITLE OF INVENTION: 222
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5;
                                                                                                                                        COMPUTER TRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC Compatible
CORPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/260,190
CLASSIFICATION NUMBER: US 08/538,701
FILING DATE: 01-MAR-1999
CLASSIFICATION NUMBER: US 08/538,701
FILING DATE: 13-MAR-1996
ATPONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/614,764
APPLICATION NUMBER: 39,804
REGISTRATION NUMBER: 39,804
REGISTRATION NUMBER: 39,804
REGISTRATION NUMBER: 39,804
RELECOMMUNICATION INFORMATION:
TELEFAN: (415) 576-0300
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TVENT: SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 3; Pred. No. 1.3e+05;
                                                Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                     STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-487-006-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KSWY 6
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COCATION: 1..6

COTHER INFORMATION: acids."

FEATURE:

NAME/KEY:

COTHER INFORMATION: acids."

NAME/KEY:

COTHER INFORMATION: focte= "Amino acid is amidated at LOCATION: 6 OTHER INFORMATION: the C-terminal."

OTHER INFORMATION: the C-terminal."

OUGEY Match

GUEST LOCAL Similarity 75.0%; Pred. No. 1.3e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 SWYF 7

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Db 3 SWWF 6

Search completed: January 17, 2001, 13:47:42 -
Job time: 241 sec
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/ Search time 43.61 Seconds
(without alignments)
7.057 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      268485 segs, 34193795 residues
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               January 17, 2001, 13:42:21
                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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49
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                                                                                                                               1 MAPTKDEFD 9
                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                           Title:
Perfect score:
                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                Sequence:
                                                                                                                                                                                      Searched:
                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Factor VIII antige	Cadherin-8 cell ad	Cadherin-15 cell a	Human TSH receptor	Human ventricular	Human leucocyte an	Cytotoxic T lympho	Peptide from P.fal	Immuno-reactive pe	Immunogenic peptid	Specific human leu	Cadherin-15 cell a
SUMMARIES	QI	R90950	Y61841	Y62453	R73400	R10267	W49525	R43246	W54664	W48987	Y09316	W43880	Y62517
	DB	17	21	21	16	12	17	14	13	13	20	18	21
	Query Match Length DB	σ	5	S	æ	6	6	80	8	8	80	σ	S
	Query	100.0	49.0	9.0	0.6	49.0	9.0	6.9	46.9	6.9	6.9	6.9	4.9
æ	S S	10	4	4	4	4	4	4	4	4	4	4	4
	Score	49	24	24	24	24	24	23	23	23	23	23	22
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PB-cadherin cell a	102 plasaodlum sv	Cytotoxic T cympho	Plasminogen active	P. falciparum circ	Borna disease viru	Peptide from F.fat	- ě	Human Item to	g) 11.48	SCP-1 in binding	OB-cadherin co.1 a	OB-cadherin rell :	Cadherin-6 cell let	PB-cadherin cer: a	N-terminal of hti-t	٠	Peptide derived 1:	Endocarditis speci	Insulin-like grow	epi tog	Peptide dorived fr	Partiul poptide 27	Multidomain prote:	-like	in-L	·like	Insulin-like growt	deriv	de	deriv	(38)	Peptide (68) inhia
X62867	R12310	R43245	W21394	R78840	R98613	W54663	Y03662	W49542	W97963	Y76701	Y73631	Y60717	Y61148	Y62852	P82888	R36869	R43613	R79640	R36899	R43460	R43643	R58438	R95061	R36870	R36895	R36915	R36923	R43590	R43614	R43639	R57538	R57568
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13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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          Peptides R90945-64 are derived from the factor VIII protein, esp. from a modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to von Willebrand factor, esp. antibodies, thus preventing or treating immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion
                                                                                                                                                                                                                                                                                                                                                             Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin.5; cadherin.5; cadherin.7; cadherin.8; cadherin.12; cadherin.12; cadherin.18; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmoglein; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, cheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                        Cadherin-8 cell adhesion recognition cyclic peptide SEQ ID NO:1679
                                                                                                                                                          ;
0
                                                                                                                                  Length 9;
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                                                                                                                        100.0%; Score 49; DB 17; 100.0%; Pred. No. 2.1e+05; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 177; 252pp; English.
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                                                                                                                                                                                                                                                                Y61841 standard; Peptide; 5 AA.
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98US-0187859.
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                                                                                                                                                          Conservative
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Matches 9; Conserv
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Modified-site
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06-NOV-1998;
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                                                                                                Sequence
                                                                                                                                  Query Match
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                                                                                                                                         angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessal regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for reducing sear tissue, or enhancing athesion of foreign tissue in a mammal. They can also be used for treating search in a mammal. They can also be used for treating and is the single can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The
                                                                                                                                                                                                                                                                                                                                                                                                       products can also be used for detection and diagnosis and in bioreactors. V60592 to Y64572 represent specifically claimed peptides, and Y64573 to Y64643 and 233183 to c. 233186 represent sequences used in the exemplification of the present invention.
                                                                                                    'nг
                        nonclassical cadherin-mediated functions. They can be used for t.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "the terminal residues are condensed with each
    other to form a cyclic peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cadherin-15 cell adhesion recognition cyclic peptide SEQ ID Nºº 118
The MAS can be used for modulating
ted functions. They can be used for
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Pred No. 2.1e+05;
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(ADHE-) ADHEREX TECHNOLOGIES INC.

Wed Jan 17 15:02:14 2001

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Gaps

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Length 8; Indels

Score 24; DB 16; L Pred. No. 2.1e+05; 1; Mismatches 2;

49.0%; 57.1%;

AV;

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Peptides with affinity to human TSH (thyroid stimulating horners) receptor antibody are used for detection of the antibody. (See also R73201-592).
                                                            Novel polypeptide(s) having affinity for the human TSH receptor
                                                                                       antibody - used in detection of the TSH antibody
                                                                                                                                                 Example 1; Page 31; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R10267 standard; Protein; 9 AA.
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WPI; 1995-167251/22.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressing cell, preventing or treating obesity in a manmal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of disease, conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bloreactors. Y60592 to Y64572 represent specifically claimed peptides, and Y64573 to Y64543 and 233183 to 233186 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                              comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, an animal, inhibiting metastasis of a cancer in a mammal, inhibiting anglogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                              New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thyroid stimulating hormone receptor; TSH; human; Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                  The present invention describes cadherin modulating agents (MA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 21; Length 5;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MITP ) MITSUBISHI PETROCHEMICAL CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TSH receptor (residues 399-406)
                                                                                                                                                                                                                                                                                            60; Page 188; 252pp; English
                              Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R73400 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; affinity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93JP-0240853
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                                 Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KDEFD 9
                              Blaschuk OW,
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| kdkfd !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                      disease
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                                                                                                                                                                                                                                                                                            Claim
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(first entry)

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carrier, esp. by a thiolether linkage to a cysteine residue added to the C-terminal or A-terminal end of the peptides, and used as immunogens in animals to produce immune lymphocytes.

A pure monoclonal antibody is capable of forming an immune complex with NVM LC-1 and has no capability of forming an immune complex buman fast skeletal myosin LC-1.

NVM LC-1 is diagnostic of myocardial infarction or other cardiomyuopathies.
                                                Human ventricular myosin light chain-1; antigen; monoclonal antibody;
immunoassay; myocardial infarction; diagnosis; cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monocional antibody to human ventricular myosin light chain-1 used in immunoassays to diagnose myocardial infarction or other cardio-myopathies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
Human ventricular myosin light chain-1 antigen (11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.0%; Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 16; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsueda
                                                                                                                                                                                                                                                                                                                    90WO-US03434
                                                                                                                                                                                                                                                                                                                                                                              89US-0366913,
                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHO-) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicol PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-022323/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA;
                                                                                                                                                                                                                                                                                                                    14-JUN-1990;
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W49525;

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RESULT W49525

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Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;
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                                                                                                                                                                                                                                                                                                                    The sequence is that of peptide cp29 which is recognised by, or can induce, cytotoxic T lymphocytes. It may be useful in vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mannose
in,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Increasing uptake and presentation of antigen(s) - by adding residue(s) to antigen for increasing T cell response, useful e.g. vaccines against viral infection(s)
                                                                                                                                                                                                               Peptide(s) recognising or inducing cytotoxic T lymphocytes useful in vaccines against malaria or \rm HIV^2, derived from specific antigen and human leukocyte antigen contg. class I
                                                                                                                                                                                                                                                                                                                                                                                                                           46.9%; Score 23; DB 14; Length 8; 66.7%; Pred. No. 2.1e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                       HC;
                                                                                                                                                     Whittle
                                                                                                                                                       McMichael AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide from P.falciparum CSP 368-375 b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 29; 47pp; English
                                                                                                                                                                                                                                                                                         Claim 6; Page 30; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W54664 standard; peptide; 8 AA.
                                                                                                                                                     Hill AV,
                                                93WO-GB00711
                                                                            92GB-0008068
92GB-0017704
                                                                                                                       (ISIS-) ISIS INNOVATION LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drijfhout JW, Koning F;
                                                                                                                                                     Gotch FM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-230631/20.
                                                                                                                                                                                   WPI; 1993-336833/42
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; treatment.
                                                                                                                                                                                                                                                            restricted epitope
                                                                                                                                                                                                                                                                                                                                                                                 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TKDEFD 9
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2 skdeld 7
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                                                05-APR-1993;
                                                                            03-APR-1992;
20-AUG-1992;
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                    14-0CT-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                     Elvin J,
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This peptide is an example of a peptide which binds to a human leucocyte artigen HLA-DD4 molecule. The peptide was isolated from a phagemid combinatorial library comprising the sequence V05953, by screening with an HLA-DD4 molecule. The peptide is used for the treatment of autoimmune disease, or especially for treatment of viral diseases.
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-binding oligopeptide and an immuno:regulator contg it - used in the treatment of auto:immune disease
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                  Indels
                                                                                                                                                                                                                                                                       Human leucocyte antigen; HLA-DQ4; combinatorial library; autoimmune disease; chronic articular rheumatism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytotoxic I lymphocyte recognition/induction peptide.
   Pred. No. 2.1e+05;
0; Mismatches 2;
                                                                                                                                                                                                                                         Human leucocyte antigen DQ4 binding peptide #416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTL; vaccine; malaria; specific antigen-derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 47; 61pp; Japanese.
                                                                                                                                                  W49525 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R43246 standard; peptide; 8 AA.
   71.48;
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                                                                                                                                                                                                             05-JUN-1998 (first entry)
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserv
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1 mapkkpe 7
                                             1 MAPTKDE 7
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aptkek
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                                                                                                                                                                                                                                                                                                                    Synthetic.
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R43246;

RESULT

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Indels

100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0;

Best Local Similarity 100. Matches 4; Conservative

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RESULT 10
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(preferably 2) mannose can be attached to increase their uptake as antigens by antigen-presenting cells. Uptake of agonist mannosylated peptides will increase the T cell response, whereas uptake of antagonist peptides blocks the T cell response. Blocking binding of immunogenic autoantigens can be used in treatment of type I diabetes, rheumatoid arthritis, graft rejection etc., also to induce T cell non-responsiveness. Vaccines containing mannosylated antigen are used to prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present peptide is an immunogenic epitope which is recognised by the CD8+ class I major histocompatibility complex (MHC) restricted cytocoxic T-lymphocytes of patients harboring latent HCMY infection. If the peptide is claimed to be capable of activating cytotoxic T-cell lymphocytes in the absence of active viral replication, and thus is useful for eliciting a cellular immune response against HCMV by normal and immunodeficient subjects. The immunological peptide can also be formulated as a vaccine which is claimed to be useful for protecting against HCMV infection, augmenting the immune system response to a HCMV infection or protecting against reactivation of a latent HCMV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic epitope; human cytomegalovirus; HCMV; vaccine; CTL;
CD8+; cytotoxic T-lymphocyte; MHC; major histocompatibility complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoreactive human cytomegalovirus epitopes - useful to vaccinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immuno-reactive peptide CTL epitope 4 of human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 19; Length 8;
Pred. No. 2.1e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 48; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W48987 standard; peptide; 8 AA.
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66.78;
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96US-0747488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CITY ) CITY OF HOPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-297862/26.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                         8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                              and parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TKDEFD 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :111 1
2 skdeld 7
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12-NOV-1996;
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                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W48987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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DB 19; Length 8;

46.9%; Score 23;

Query Match

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The present invention describes immunologically active peptides (1APs) capable of eliciting a cellular immune response to human cytom. Interiors (NCW). The IAP can be used in a (cellular) vaccine to augment the immune system response to HCW, or to provide immunity against HCW. The immune system reactivation. Or to provide immunity against HCW rhe IAP (cellular) vaccine can also protect an individual having a laterior in the presence or absence of HCWV-infected T lymphocytes. The viral vector containing IAP encoding DNA can also be used to provide immunity against HCWY. The IAP can be used to prepare HCMY rearritive human cytotoxic T lymphocytes. The antigen presenting cells primed with the IAPs can be used as diagnostic reagents to detect immunostimulation by HCMY. They can also detect active HCMY infection or exposure to HCMY on cause opportunistic infections resulting in a variaty of complications in, e.g. immunosuppressed patients. The IAP vaccines impart immunity to bone marrow transplant recipients, solid organ recipients, heart patients, AIDS patients or women of child-bearing years, without the need for ex vivo expansion of HCMY-specific cytoloxic I lymphocytes (which requires sophisticated laboratory setup and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ö
                                                                                                          Immunogenic peptide cytotoxic T lymphocyte epitope SEQ 11 MO:9 of hally.
                                                                                                                                             Human cytomegalovirus; hCMV; immunologically active peptide; vaccine; immune response; cytotoxic T lymphocyte; CTL; immunostimulation; infection; immunosuppression; bone marrow transplant; solid organ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic peptide cytotoxic T lymphocyte epitopes of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 100.0%; Score 23; DB 20; I Similarity 100.0%; Pred. No. 2.1e+05; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 49; 64pp; English.
Y09316 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                           98WO-US09652.
                                                                                                                                                                                                                                                                                                                                                                                                            98US-0021298
97US-0950064
                                                                     08-JUL-1999 (first entry)
                                                                                                                                                                                                                                              Human cytomegalovirus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CITY ) CITY OF HOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         York J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-277590/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytomegalovirus
                                                                                                                                                                                                                                                                                                  WO9919349-A1.
                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                14-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diamond DJ,
                                                                                                                                                                                                         heart; AIDS.
                                                                                                                                                                                                                                                                                                                                       22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                    X09316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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nonclassical cadherin mediated cell adhesion;

(first entry)

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inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; uneurological disease; cyclic.
                        Cadherin-15 cell adhesion recognition cyclic peptide SEQ ID NO:2183.
                                                                                                                                                                                                                                                                                                                                                                               (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-038791/03.
                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                     Blaschuk OW,
  02-MAR-2000
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                W09957149-A2
                                                                                                                                                                                                                                                                                               05-MAY-1999;
                                                                                                                                                                                                                                                                                                                     05-MAY-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                        08-MAR-1999;
                                                                                                                                                                                                                                                                        11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                            20-JAN-1999
                                                                                                                                                      Synthetic.
  The present sequence represents a specific example of an immunogenic peptide which was used in a new method of inducing a cytotoxic T cell (CTL) response against a preselected antigen in a patient. The method comprises contacting CTLs from the patient with the immunogenic peptide (containing defined motifs) which binds one of the four HLA MHC products HLA-A3.2, HLA-A1, HLA-A11 or HLA-A3.4.1, the peptide having a dissociation constant (Kd) of less than 5 x 10-7 M. Immunogens are viral, e.g human immunodeficiency virus type I (HIV-1), hepatitis B virus (HBV) and hepatitis C virus (HCV) or cancer antigens and are used in vaccines for the prevention and treatment of viral infection and cancer. The immunogens may be administered to the patient as a nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                       Specific human leukocyte antigen binding peptide - used in vaccines for the treatment and prevention of e.g. bacterial or viral
                                                                                                                                                                           leukocyte antigen; HLA; vaccine; bacterial infection; viral;
                                                                                                                                                  Specific human leukocyte antigen binding peptide #84
                                                                                                                                                                                       cytotoxic T-cell; CTL; immunogenic peptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 18; L
Pred. No. 2.1e+05;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                              Sette A;
                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 39; 49pp; English.
                                                                             W43880 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                             Grey HM, Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                            97WO-US04451
                                                                                                                                                                                                                                                                                                                   97US-0821739
                                                                                                                                                                                                                                                                                                                              96US-0013833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the peptide (gene vaccine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                infection and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                             20-APR-1998
                                                                                                                                                                                                                                              WO9734617-A1
                                                                                                                                                                                                                                                                                            21-MAR-1997;
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21-MAR-1996;
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             ||||
2 ptkd
                                                                                                                                                                                                             Synthetic.
PTKD
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                                                                                                      W43880;
                                                         RESULT 11
                                                                    W43880
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Byers S;

Gour BJ,

98US-0073040. 98US-0187859. 99US-0234395. 99US-0264516.

99WO-CA00363.

//note= "the terminal residues are condensed withoute" other to form a cyclic peptide"

Location/Qualifiers

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The present invention describes cadherin modulating agents (MA)

comprising peptides which comprise a nonclassical cadherin cell adhesion

cecognition (CAR) sequence. The MAs can be used for modulating

crecognition (CAR) sequence. The MAs can be used for modulating

crecognition (CAR) sequence. The MAs can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a

comman, enhancing delivery of a drug to a tumour in a mammal, treating cancer in

cenhancing delivery of a drug to a tumour in a mammal, inhibiting

compressing cell, preventing or treating obesity in a mammal, simmilating

concressing vasopermeablisty in a mammal, enhancing drug delivery to the

central nervous system, treating a demyelinating neurological disease,

increasing vasopermeablisty in a mammal, enhancing and disease,

conclassical cadherin-expressing cells, inhibiting synaptic stability in

a mammal, or preventing pregnancy in a mammal. They can also be used for

cor reducing scar tissue, or enhancing adhesion of foreign tissue, or

conclasted macular degeneration, multiple sclerosis and diabetes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             products can also be used for detection and diagnosis and in
Dioreactors. 760592 to 764572 represent specifically claimed peptides,
and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
exemplification of the present invention.
New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                          Claim 60; Page 188; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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Gaps

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. Y62517 standard; Peptide; 5 AA.

RESULT 12

Y62517;

X ID

6

2 APTKDEF 8 | || || 3 agtkqef

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Length 9; Indels

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DB 21; Length 5;
44.9%; Score 22;
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Query Match

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                                                                                                                                                                                                                    111 |
1 kdeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1991
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                                                                                                                                                                                                      5 KDEFD
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                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                           R12310;
                                                                                                                                                                                                                                                                                                                                                                                         hybrid
                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes cadherin modulating agents (MA) compriss a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, a mammal, inhibiting an amammal, inhibiting a mammal, inhibiting a mammal, inhibiting expressis of a cancer in a mammal, inhibiting expressis in a mammal, inhibiting expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing delivery to the central nervous system, treating a demyelinating neurological disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in
                                                                                                                                                                                                           Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-7; cadherin-8; cadherin-12; cadherin-12; cadherin-12; cadherin-13; T-cadherin; PB-cadherin; desmoglein; desmoglein; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                       /note= "the terminal residues are condensed with each
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                      PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:2423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cadherin modulating agents, used for modulating nonclassical
                  ö
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                    other to form a cyclic peptide'
     Pred. No. 2.1e+05;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 72; Page 194; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Byers S;
                ó
                                                                                                                    Y62867 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0187859.
99US-0234395.
99US-0264516.
     80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-CA00363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0073040.
                                                                                                                                                                 (first entry)
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-038791/03
                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                       KDEFD 9
                                                           1 kdeld 5
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                           WO9957149-A2
                                                                                                                                                                 02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 11-NOV-1999
                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease
                                                                                                                                            Y62867;
                                                                                              13
                                       'n
                                                                                             RESULT
                                                                                                          X62867
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a mammal, or preventing pregnancy in a mammal. They can ..1so be used for e.g. enhancing or directing neurite outgrowth, facilita, ..., wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue. In a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. Y60592 to Y6572 represent specifically claimed peptides, and Y64573 to Y6643 and 231186 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ing region of the CS protein of plasmodium. It can be used in a vaccine for protection against malaria. The peptide is pref.linked to a 2nd peptide from the 1st flanking domain and the resulting polypeptide fused to a carrier protein, e.g tetanus toxoid, diptheria toxin or cholera B toxin. A preferred vaccine comprises 81 N-terminal AAs of the influenza virus nonstructural protein 1 (NSIB1), fused, via a synthetic linker, to a 1st flanking region of the CS protein, which is itself fused to a 2nd flanking region of the CS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The peptide is a sporozoite neuralising epitope from the 2nd flank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide comprising immunogenic determinants from P talciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 21;
Pred. No. 2.1e+05;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Page 16; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R12310 standard; Protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID2 plasmodium surface peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0447746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90EP-0313257
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-179771/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                     5 AA;
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                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide(s) recognising or inducing cytotoxic T lymphocytes - useful in vaccines against malaria or HIV-2, derived from specific antiqen and human leukocyte antiqen contg. class I restricted epitope
 44.9%; Score 22; DB 12; Length 8; 80.0%; Pred. No. 2.1e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.9%; Score 22; DB 14; Length 8; 80.0%; Pred. No. 2.1e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Elvin J, Gotch FM, Hill AV, McMichael AJ, Whittle HC;
                                                                                                                                                                                                     Cytotoxic T lymphocyte recognition/induction peptide.
                                                                                                                                                                                                                              CTL; vaccine; malaria; specific antigen-derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 30; 35pp; English.
                                                                                                                              R43245 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                          93WO-GB00711.
                                                                                                                                                                                                                                                                                                                                                92GB-0008068.
92GB-0017704.
                                                                                                                                                                               04-MAY-1994 (first entry)
Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-336833/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8 AA;
                                                              ||| |
| kdeld 8
                                                                                                                                                                                                                                                                                                                          05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                03-APR-1992;
20-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| |
3 kdeld 7
                                               5 KDEFD 9
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                                                                                                                                                                                                                                                    Synthetic.
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R43245
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Search completed: January 17, 2001, 13:42:22 Job time: 136 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:43:36; Search time 36.59 Seconds (without alignments) 16.701 Million cell updates/sec Run on:

US-08-765-837-6 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1 MAPTKDEFD 9

Sequence:

195891 segs, 67900655 residues Searched:

787 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	script	alpha-2-macroqlobu	alpha-2-macroglobu	hypothetical prote	carbon-monoxide de	neuropeptide TE-6	orf 3 rara 5'-reqi	еаш	ribulose-bisphosph	T-cell receptor be	ATPase R1 subunit	calliFMRFamide 3 -	calliFMRFamide 5 -	Iq kappa chain C r	ptidylg	repetitive protein		calliFMRFamide 10	calliFMRFamide 2 -	unidentified 48.7K	T-cell receptor be	calsequestrin, fas	calliFMRFamide 4 -	triacylglycerol li	cellulase (EC 3.2.	trypsin (EC 3.4.21	τ	tyrosine protein k		starvation-induced
	ID	S66635	866636	D41654	PL0139	JH0784	S15596	B41983	PS0324	PT0530	D48186	C41978	E41978	B38740	A42266	B60110	S29272	A44787	B41978	PC7078	PH0937	B39040	D41978	S57274	S21273	A61328	A41978	178890	90	S53508
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proctolln Americ	anglotensin-conver	fulicin - glant Af	proctolin - Atlant	T-cell receptor be	MHC H2-L antigen -	T-cell receptor be	T-cell receptor be	opacity protein P.	CalliFMRFamide 11	hucolin, 75K chain	angiotensin-conver	citrate synthase -	glucose-6-phosphat	158K excantigen -	alcohol dehydroyen
новона	PQ0009	A44692	A60411	PT0656	I65546	PT0510	PT0599	S16365	B44787	568004	A31570	S53008	S11078	B33099	871919
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24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5
12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12

ALIGNMENTS

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Johns 2-macroglobulin isoform 1 - bovine (fragment)
C; Species: Bos primigenius indicus (zebu cattle)
C; Species: Bos primigenius indicus (zebu cattle)
C; Species: Bos primigenius indicus (zebu cattle)
C; Saccession: S66635
R; Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sut FEBS Lett. 372, 93-95, 1995
A; Fiele: Crystallisation and preliminary X-ray analysis of the receptor-binding domain A; Reference number: S66635
A; Reference number: S66635
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-9 cDoL>
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; 0 Caps ; 0; Indels h 44.9%; Score 22; DB 2; Length 9; Similarity 100.0%; Pred. No. 2e+05; 4; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 4; Conserv

5 KDEF 8 õ οp

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alpha-2-macroglobulin isoform 2 - bovine (fragment)
C;Species: Bos primigenius indicus (zebu cattle)
C;Species: Bos primigenius indicus (zebu cattle)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 17-Mai-1999
C;Accession: S66636
R;Dolmer, R.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Son FBRS Lett. 372, 93-95, 1995
FBRS Lett. 372, 93-95, 1995
FBRS Lett. 372, 93-95, 1995
A;Title: Crystallisation and preliminary X-ray analysis of the rec:pror-binding domain A;Reference number: S66636
A;Accession: S66636
A;Accession: S66636
A;Molecule type: protein
A;Residues: 1-9 <DOL>

Gaps ; 44.9%; Score 22; DB 2; Length 9; 80.0%; Pred. No. 2e+05; Live 0; Mismatches 1; Indels Query Match
Best Local Similarity 80.0
Matches 4; Conservative

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| ||| PKKDE 9 3 PTKDE 7 ò

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RESULT D41654

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C;Species: Homo sapiens (man)
C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C;Accession: S15596
C;Accession: S15596
R;Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A;Title: Characterization of a functional promoter for the human retinoic acid recept A;Reference number: S15594; MUID:91088249
A;Accession: S15596
                                                                                                                                                                                                                                                                                                                                                                                                           entry HSRARA2, release 111.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS0324
ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orf dowstream to bacterioferritin - Azotobacter vinelandii (fragment)
C; Species: Azotobacter vinelandii
C; Species: Azotobacter vinelandii
C; Species: Azotobacter vinelandii
C; Azotobacter vinelandii
C; Azotobacter vinelandii
C; Azotobacter vinelandii
R; Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
A; Title: Unification of the ferritin family of proteins.
A; Reference number: A41983; MuID: 92196129
A; Accession: B41983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M03692; NID:g142297; PIDN:AAA22122.1; PID:g142299
A;Note: sequence extracted from NCBI backbone (NCBIP:88442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid; protein
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                                                                                                                                                                                                                                                                                                                                                                                                           in GenBank
translated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 2;
Pred. No. 2e+05;
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Pred. No. 2e+05
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             A. Cross-references: EMBL:X56058; NID:935876
A.Note: this ORF from Fig. 2 is not annotated
C. Comment: This sequence is not thought to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:RARA
A;Cross-references: GDB:120337; OMIM:180240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.7%;
75.0%;
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60.0%;
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Best Local Similarity 75.0°,
..t.hes 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-9 <GRO>
A;Cross-references: GB:M83692;
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                                                                                                                        orf 3 rara 5'-region - human
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Best Local Similarity
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                                                               C;Accession: D41654
R;Kroll, J.S.; Langford, P.R.; Loynds, B.M.
Bacteriol. 173, 7449-7457, 1991
A;Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para A;Reference number: A41654; MUID:92041655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: PL0139
R; Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Rrch. Microbiol. 152, 335-341, 1989
A; Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop A; Reference number: PL0138; MUID:90055678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydoflava (fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuropeptide TE-6 - pig roundworm (fragment)
C;Species: Ascaris suum (pig roundworm)
C;Species: Ascaris suum (pig roundworm)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 28-Apr-1995
C;Accession: JH0784
R;Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan, R Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992
A;Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascaris A;Reference number: JH0784; MUID:93038603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: 2-Met is also found
C;Comment: Cardon-monoxide dehydrogenase consists of three polypeptide chains: large,
C;Keywords: oxidoreductase
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hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
C;Species: Haemophilus parainfluenzae
C;Date: 12-Jun-1992 #text_change 24-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Pseudomonas carboxydoflava
.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 2e+05;
0; Mismatches
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Pred. No. 2e+05;
1; Mismatches 1
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1; Mismatches
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60.0%;
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50.08;
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ilarity 75.0%;
Conservative
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A; Residues: 1-6 cSMA-
A; Experimental source: gonoduct
C; Keywords: neuropeptide
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Best Local Similarity 60.v.
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Mètches 3; Conserv
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A; Molecule type: DNA
A; Residues: 1-4 <KRO>
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RESULT 12
64.1978
calliFMRFamide 5 - bluebottle fly (Calliphora vomitoria)
C.Species: Calliphora vomitoria
C.Species: Calliphora vomitoria
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-M.r-1999
C.Accession: E44978
R.Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; F., Feld, J.F.; Tho Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A; Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 Hearton number: A41978; MUID:92196111
A; Accession: E41978
A; Molecule type: protein
A; Residues: 1-9 < DUV>
C; Keywords: amidated carboxyl end; neuropeptide
F; 9/Modified site: amidated carboxyl end (Phe) #status experimental.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain C region (PY20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mai-1998
C;Date: 19-Mar-1997 #sequence contains the chain solution of the chain solution of the chain solution of the chain solution of the chain variable region sequences and antibody properties of the chain solution of the 
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-Nii-2 neuropepthd...;
A;Reference number: A41978; MUID:92196111
A;Accession: C41978
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 < Duv > Cykeywords: amidated carboxyl end; neuropeptide
C;keywords: amidated carboxyl end (Phe) #status experimental.
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                                                                                                                                                                                                                                                                                                                     Length 9;
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60.0%; Pred. No. 2e+05;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                     Score 16; DB 2;
Pred. No. 2e+05;
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40.0%;
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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A; Molecule type: mRNA
A; Residues: 1-9 <RUF>
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| APGQD :
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1 SPSQD
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C;Species: Calliphora vomitoria
C;Species: Calliphora vomitoria
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: C41978
R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPASE RI subunit - wood tobacco (fragment)
(Species: Nicotiana sylvestris (wood tobacco)
C.bate: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C.Accession: D40186
R.De Paepe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Scl. US.A. 90, 5934-5938, 1993
A.Title: Specific mitochondrial proteins in pollen: presence of an additional ATP syntha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell receptor beta chains have few N regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0530
B;Feeney, A.J.
J; Exp. Med. 174, 115-124, 1991
A;File: Junctional sequences of fetal T cell receptor beta chains have few A;Reference number: PT0539
A;Accession: PT0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                       Length 5;
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A.Residues: 1-9 CDE1-
A.Experimental source: pollen
A.Note: sequence extracted from NCBI backbone (NCBIP:134871)
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0
                                                                                       DB 2;
2e+05;
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100.0%; Pred. No. 2e+05;
iive 0; Mismatches 0
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Pred. No. 2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: adult thymus, strain BALB/c C; Keywords: T-cell receptor
                                                                                       Score 16; DB 2; Pred. No. 2e+C 0; Mismatches
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      A; Experimental source: leaf, chlorophyll
                                                                     32.7%; Scor.
100.0%; Pre
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60.0%;
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A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
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Matches 3; Conserv
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Matches 3; Conserv
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5 LAPYK 9
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4 APT 6
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peptidylglycine monooxygenase (EC 1.14.17.3), rPAM-5 - rat (fragment)
N;Alternate names: peptidylglycine alpha-amidating monooxygenase
N;Alternate names: peptidylglycine alpha-amidating monooxygenase
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A42266
C;Accession: A42266
A;Reference number: B.A; Green, C.B.; Campbell, T.A.; Stoffers, D.A.; Keutmann, H.T.; Mains, R.E.
A;Title: Alternative splicing and endoproteolytic processing generate tissue-specific fc
A;Reference number: A42266
A;Reference number: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Trypanosoma cruzi
C; Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993
C; Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993
C; Ccession: B60110
R; Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E. Infect. Immun. 57, 1959-1967, 1989
A; Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A; Reference number: A60110; MUID: 89277508
A; Reference number: A60110
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: Te C < < COF>
A; Note: this is an example of a five residue tandem repeat from this protein; the actual C; Keywords: tandem repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 2; Length 9;
Pred. No. 2e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.7%;
Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 75.0%;
Matches 3; Conservative
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6 KDTF 9
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2 APKK 5
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Search completed: January 17, 2001, 13:43:37 Job time: 156 sec

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January 17, 2001, 13:47:09 ; Search time 20.9 Seconds (without alignments) 13:907 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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49
1 MAPTKDEFD 9
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Perfect score:
Sequence:
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Total number of hits satisfying chosen parameters:

88757 seqs, 32294092 residues

Searched:

213

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITMMADIES

	scription	P80632 zea mays (m	psen		P25825 azotobacter				P80488 thiobacillu				_	P13071 citrobacter				P31890 ascaris suu	P41866 calliphora				P41492 sarcophaga	P42998 eisenia foe	P81736 leucophaea		homo		P24272 vibrio fisc	,	991	3973	13737 mytilus e	P41871 helisoma tr
SUMMARIES	ΩI	UC26_MAIZE	DCML_PSECF	FAR1_ASCSU	YBFR_AZOVI	FAR3_CALVO	FAR5_CALVO	TKC1_CALVO	CLP_THICU	FAR2_CALVO	FARA_CALVO	FAR4_CALVO	FAR1_CALVO	BIOA_CITFR	BIOA_SALTY	PRCT_PERAM	TMOF_SARBU	FAR2_ASCSU	FARB_CALVO	ACI_THUAL	PLP_BRANA	FAR5_ASCSU	NSK1_SARBU	OXYT_EISFO	TRP4_LEUMA	UF02_MOUSE	UHA2_HUMAN	UPA3_HUMAN	LUXE_VIBFI	BPP7_BOTIN	SUGA_ACHDO	TRM3_ECOLI		FAR1_HELTI
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di	Query Match	36.	36.7	34.7	34.7	32.7	32.7		30.6				26.5						24.5								24.5		22.4	22.4	22.4	22.4	22.4	22.4
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			ite) COLEOPTILE	Tracheophyta; eae; Zea.	=		54;	Length			.2 Q jt
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とと8800000004		STANDARD;		c). :idiplantae; E Liliopsida;	[1] SEQUENCE. TISSUE-COLEOPTILE; Touzet P., Riccardi F., Morin C., Damer Pernollet JC., Zivy M., de Vienne D.; The maize two dimensional gel protein	genome analysis program."; Theor. Appl. Genet. 93:997-1005(1996) Theor. Appl. Genet. 93:997-1005(1996) PROTELN IS: 7.0, ITS MW IS: 57.2 MAIZE-2DPAGE; P80632; COLEOPTILE.	8 90 MW	36.79 42.99 vative			PSECF DOML_POSECE STANDARD; PRT; 9 AA P19913; 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 01-DEC-1992 (Rel. 24, Last sequence update) 01-DEC-1992 (Rel. 24, Last annotation updat. CARBON WONOXIDE DEHYDROGENASE LARGE CHAIN (Pseudomonas carboxydoflava. Bacteria; Proteobacteria; beta subdivision; [1] FAUTOGENORE. SEQUENCE. Kraut M., Hugendieck I., Herwig S., Meyer O "Homology and distribution of CO dehydrogena carboxydotrophic bacteria."; Arch. Microbiol. 152:335-341(1989).
		ANI	34, 34, 38,	pla lic	di Ziv	632,00	99				ANE 17 17 24 24 24 32 32 32 32 32 32 32 32 32 32 32 32 32
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100111111111111111111111111111111111111		IZE	01-001-1996 (Rel. 34, 01-001-1996 (Rel. 34, 15-JUL-1999 (Rel. 38, UNKNOWN PROTEIN FROM	(Frackent); Zea mays (Maiz Eukaryota; Vir Magnoliophyta;	[1] SEQUENCE. TISSUE-COLEOPTILE; TOUZET P., RICCALG Pernollet JC., Z	anal Appl CELI TEIN DPAG	. 🖼	h Siπ 3;	APTKDEF : :	AEPRDQF	PSECF DOML PSECF P19913; P19913; P10913; P101 FEB-1991 (R PEB-1992 (R PEB-1992 (R PEB-1992 (R PEB-1992 (R PEB-1991
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Incolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly calliphora vomitoria.";
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-!- FUNCTION: ABLE TO LICE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-THORACIC GANGLION;
BUDDLINE-292196111; PubMed=1549595;
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;
Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Length 9;
Pred. No. 8.9e+04;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION.
2F0B0699CAB6C5A7 CRC64;
                 Stiefel E.I.; "Unification of the ferritin family of proteins."; Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
                                                                                                                                                                                                                                                                                                             9 AA; 947 MW; DF98B5A1B417776D CRC64;
                                                                                                                                                                                                                                                                                                                                                               Score 17; DB 1; Pred. No. 8.9e+04; 1; Mismatches 1,
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFMRFAMIDE 3.
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                                                                                                                                                                                                                                 EMBL; M83692; AAA22122.1; -.. PIR; B41983. B41983. Hypothetical protein. 9 SEQUENCE 9 AA; 947 MW; DF
                                                                                                                                                                                                                                                                                                                                                                  34.78;
60.08;
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9 AA; 1114 MW;
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Best Local Similarity 40.0
Matches 2; Conservative
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Best Local Similarity
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1 MAPPR 5
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FAR5_CALVO
ID FAR5_CALVO
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P41858;
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FAR3_CALVO
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Neuron 2:1465-1473(1989).
-!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTORNEURONS. REDUCES THE
INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
               COFACTOR: MOLYBDENUM.
SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Ascariddida; Ascaridoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90180465; PubMed=2627377; Cowden C., Stretton A.O.W., Davis R.E.; "AFI, a sequenced bioactive neuropeptide isolated from the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MY-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
HYPOTHETICAL PROTEIN IN BFR 3'REGION (FRACMENT).
Azotobacter vinelandii.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Azotobacter.
                                                                                                                                                                                                 Score 18; DB 1; Length 9;
Pred. No. 8.9e+04;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.7%; Score 17; DB 1; Length 7; 75.0%; Pred. No. 8.9e+04; Live 1; Mismatches 0; Indels
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7 AA; 953 MW; 69D40059CB144350 CRC64;
                                                                                                                                            9 AA; 974 MW; 0224DAB6C2D76DD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last Sequence update)
01-EBB-1996 (Rel. 33, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE AFI.
                                                                                                                                                                                                                                                                                                                                                                                                     7 AA.
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SEQUENCE FROM N.A.
MEDLINE=92196129; PubMed=1549605;
                                                                                                                                                                                                   36.7%;
60.0%;
                                                                                       Oxidoreductase; Molybdenum.
                                                                                                                                                                                                   Query Match 36.7
Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
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ACCEPTOR.
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3 APVQD 7
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P25825;
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SEQUENCE
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Bacteria; Proteobacteria; beta subdivision; Comamonadaccae; Thi monas.
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Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridea; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 1; Length 8;
Pred. No. 8.9e+04;
0; Mismatches 3; Indels
                                                                                                                                                                         SEQUENCE.
STRAIN=DSM 5494;
Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
Submitted (SEP-1995) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED CHEMOLITHOTROPHICALLY.
                                                                                                                                                                                                                                                                                           785 MW; 91487B06DDC2D76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P41857;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
CALLIFMRFAMIDE 2.
                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
EMMOLITHOTROPH-SPECIFIC PROTEIN (FRAGMENT).
Thiobacillus cuprinus.
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                      B AA.
                      PRT;
                                                      (Rel. 34, Created)
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50.0%;
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Best Local Similarity 50.0%;
Matches 2; Conservative
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SEQUENCE 9 AA; 1128 MW;
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Best Local Similarity 50.0
Matches 3; Conservative
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                      STANDARD;
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01-0CT-1996 (
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P80488;
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                                                 CALLIFMRRAMIDE 5.
Calliphora vomitoria (Blue blowfly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petergota: Neoptera; Endoptergota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLITACHYNIN II.
Calliphora vomitoria (Blue blowfly).
Eukaryota, Arthropoda, Tracheata; Hexapoda; Insecta;
Detrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
Naessel D.R.;
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MEDLINE-92196111; PubMed-1549595;
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.E., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFFamides) from the blowfly
Calliphora vomitoria.";
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-: SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16; DB 1; Length 9;
Pred. No. 8.9e+04;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%; Score 16; DB 1; Length 9; Similarity 100.0%; Pred. No. 8.9e+04; 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                39D10699CAB6D867 CRC64;
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SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA.
                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.7%;
Best Local Similarity 60.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 9 AA; 1068 MW;
                                                                                                                                                                                                                                                                                                                                                             Neuropeptide; Amidation. MOD_RES 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND SYNTHESIS
                                                                                                                                                                                                                                                                                                                                             PIR; E41978; E41978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 APTKD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKC1_CALVO
P41517;
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TKC1_CALVO
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                                                  Score 15; DB 1; Length 9;
Pred. No. 8.9e+04;
2; Mismatches 0; Indels
AMIDATION.
29D00699CAB6C5A7 CRC64;
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FARA_CALVO
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)

CALLIPHREAMIDE 1.

Calliphora vomitoria (Blue blowfly).

Eukaryota: Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;

Petrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomircpha;

Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: BIOTIN BIOSYNTHESIS.
-!- SUBUNIT: HOMODIMER.
-!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
(EC 2.61.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrobacter freundii.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92196111; PubMed=1549595;

Buve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;

Rehfeld J.F., Thorpe A.;

Rinclation, Structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly Calliphora vomitoria.";

Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

-1- FUNCTION: ABLE TO INDIGE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.

-1- SIMILARITY: BELONGS TO THE FARP (EMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.5%; Score 13; DB 1; Length 9; 50.0%; Pred. No. 8.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
29D00699CAB6C6C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA; 1169 MW;
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                                                                                                                                                                                                                                                                                                                                         TISSUE=THORACIC GANGLION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropeptide; Amidation.
MOD_RES 9 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 50.0
les 2; Conservative
                                                                                                                STANDARD;
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2 PQQD 5
                     2 PNQD 5
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P13071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY
                                                                                                                                                                                                                                                                                                                       SEQUENCE.
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                                                                         RESULT 12
FAR1_CALVO
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Matches
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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                                                                                                                                                                                                                      TISSUE-THORACIC GANGLION;
MEDLIAE-92196111; PubMed=1549595;
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.E., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Calliphora vomitoria.";
Proc. Natl. Acad. Sci., U.S.A. 89:2326-2330(1992).
-I. SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92196111; PubMed=1549595;

Buve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

Reheld J.F., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
calliphora vomitoria.";

Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

-I. SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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0
                                                                                                              Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 1; Length 9;
Pred. No. 8.9e+04;
1; Mismatches 1; Indels
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Pred. No. 8.9e+04;
1; Mismatches 1; Indels
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OR S OR A.
29D00699CAB40457 CRC64;
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31730699CAB6D457 CRC64;
                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NoV-1995 (Rel. 32, Last sequence update)
01-NoV-1995 (Rel. 32, Last annotation update)
9 AA.
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 PRT;
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50.0%;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.6
Best Local Similarity 50.0
Matches 2; Conservative
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MOD_RES 9 9
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 STANDARD;
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Best Local Similarity
Matches 2; Conserv
                                                                                           CALLIFMRFAMIDE 10.
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PNRD 5
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P41859;
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 FARA_CALVO
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Starratt A.N., Brown B.E.; "Structure of the pentapeptide proctolin, a proposed neurotransmitter" Structure of the pentapeptide proctolin, a
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"Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).
-i- FUNCTION: STHUMLATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-i- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=P.AMERICANA;
MEDLINE=81225865; PubMed=6113690;
O'Shea M..., Adams M.E.;
"Pentapeptide (proctolin) associated with an identified neuron.";
Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of proctolin in the central nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-L. POLYPHEMUS;
BEDLINE-20287800; PubMed-2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%; Score 12; DB 1; Length 5; 100.0%; Pred. No. 8.9e+04; ive 0; Mismatches 0; Indels
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6AAAB1B1A6F00000 CRC64;
                                                                  Score 12; DB 1; Pred. No. 8.9e+04;
                                                                                                                                                                                                                                                                                                                                                  (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                           5 AA.
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        horseshoe crab, Limulus polyphemus.";
Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=86232789; PubMed=2872661;
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MEDLINE-76074708; PubMed=576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Life Sci. 17:1253-1256(1975).
                                                                  24.5%;
50.0%;
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Best Local Similarity 100.u
Local 2; Conservative
    582 MW;
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                              STANDARD;
                                           Query Match
Best Local Similarity
Local 2; Conserve
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PIR; A60411; A60411
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SEQUENCE 5 AA;
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      5 AA;
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21-JUL-1986 (
01-FEB-1995 (
                                                                                                                                                                                           2 TTDD 5
                                                                                                                                                                                                                                                                                                           PRCT_PERAM P01373;
                                                                                                                                                         4 TKDE 7
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                                                                                                                                                                                                                                                                                                                                                                                                                         PROCTOLIN
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    SEQUENCE
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PRCT_PERAM
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
(EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia co
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
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OXONONANOATE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
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INTERPRO; IPR000954; -.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
Blotin biosynthesis; Transferase; Aminotransferase;
Pyridoxal phosphate.
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Biotin biosynthesis; Transferase; Aminotransferase;
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STYGENE; SG10026; BIOA.
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50.0%;
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SEQUENCE 5 AA; 582 MW;
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Q9TNF1 Q9TNF0 Q9TNF3 Q9TNF2

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Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S., Karlsson G., Sodroski J., Morgado M., Galvao-Castro B., Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M., Hahn B.H.; "Molecular cloning and analysis of functional envelope guees from human immunodeficiency virus type 1 sequence subtypes A through G. The WHO and NIAID Networks for HIV Isolation and Characterization."; J. Virol. 70:1651-1657(1996).
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EMBL: U08794; AAB05175.1; -.
NON_TER
SEQUENCE 9 AA: 1098 MW; 5B76D40AB1AB01A3 CRC64;
                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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MEDLINE=95194694; PubMed=7888189;
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01-NOV-1996 (TrEMBLrel.
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TAT PROTEIN (FRAGMENT).
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Allen E.E.;
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Q70140;
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Q9n6m5 toxoplasma
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"Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene."; EMBO J. 13:3472-3480(1994).

EMBL; Z34523; CAA84282.1; -.

NON_TER 9 9

SEQUENCE 9 AA; 1047 MW; 9A8BCB07633B1045 CRC64;
                              Gaps
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                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1899;
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Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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 Score 16; DB 5; Length 8; Pred. No. 3.7e+05;
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF024717; AAB81967.1; -
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Pred. No. 3.7e+05;
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Pred. No. 3.7e+05;
1; Mismatches 4;
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MEDLINE=94341259; Pubmed=8062824;
Pahl A., Keller U.;
 32.78;
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50.0%;
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               Best_Local Similarity 33.3
Matches 2; Conservative
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Matches 4; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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TISSUB-EPIDERMIS,
WING;
MEDLINE-97165493; PubMed-9013254;
Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
"Identification and mRNA developmental profiles of two ultraspiracle isoforms in the epidermis and wings of Manduca sexta.";
Insect Mol. Biol. 6:41-51197).
EMBL; U57921; AAB64235.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
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                                                                                                                                                                                                                                                                                                                                                                     "Sequence announcement: rbcL promotor gene in Begonia formosana.";
Subaltred (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ009599; CAB52123.1; -.
EMBL: AJ009598; CAB52121.1; -.
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RBCL PROFEIN (FRAGMENY).
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcorvelidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus. NCBI_TaxID-11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fan X., DiBisceglie A.M.;
"Identification of liver specific quasispecies of the hepathtis r.
virus in chronically infected patients.";
Submitted (DEC:1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF211054; AAF30114.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14; DB 5; Length 8; Pred. No. 3.7e+05; 1; Mismatches 0; Indels
                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DIHYDROFOLATE REDUCTASE THYMIDYLATE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TRUNCATED POLYPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33CAAAA05B133044 CRC64;
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8 AA; 917 MW; BID41AFAF7776DCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%; Score 14; DB 12; ilarity 42.9%; Pred. No. 3.7e+05; Conservative 0; Mismatches 4;
                                                                                       8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA.
                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                 Housekeeping Genes.";
J. Parasitol. 0:0-0(2000).
BMBL; AF249695; AAF79153.1; -.
EMBL; AF249692; AAF79150.1; -.
EMBL; AF249693; AAF79151.1; -.
EMBL; AF249694; AAF79151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.6%;
llarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1
8 8
8 AA; 1035 MW;
                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus
                                                                                                                                                                                                                     Toxoplasma gondii
                                                                                                                                                                                                                                                                   NCBI_TaxID=5811;
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1 MLPFGDK 7
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                                                                                                                                                                                                                                                       Toxoplasma.
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SEQUENCE
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SEQUENCE
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                                                                                                          Q9N6M5;
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Q9J205
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                                                                                                                                                                                                                                                                                                                                MEDLINE-96189275; Pubwed-8605312; Joshi C.P., Kumar S., Nguyen H.T.; Joshi C.P., Kumar S., Nguyen H.T.; Application of modified differential display technique for cloning and sequencing of the 3' region from three putative members of wheat HSP70 gene family."; Plant Mol. Biol. 30:641-646(1996). EMBL: L41507; AAB02333.1; EMBL: L41505; AAB02333.1; EMBL: L41506; AAB02332.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                               Triticum aestivum (Wheat).
Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-20145478; PubMed=10679249;
Lin C.S., Lau A., Tu R., Lue T.F.;

"Identification of three alternative first exons and an intronic promoter of human PDE5A gene.";

Biochem. Biophys. Res. Commun. 268:596-602(2000).

EMBL; AFIS5195; AFR153195; AFR153195; AFR153195.
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                                                                                Q42507 PRELIMINARY; PRT; 8 AA. 01-807-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) HEAT SHOCK PROPEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEWBLrel. 15, Created)
01-0CT-2000 (TrEWBLrel. 15, Last sequence update)
01-0CT-2000 (TrEWBLrel. 15, Last annotation update)
CGMP-SPECIFIC PHOSPHODIESTERASE PDE5A2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA; 886 MW; 71B2CB1B10532768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 8 AA; 908 MW; E8A33AA879D76726 CRC64;
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Best Local Similarity 42.9%;
Matches 3; Conservative
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SEQUENCE
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Q9P0K3;
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TISSUE=PLACENTA;
Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
                                                                                                                                                                                                                                                 Romaniec M.P., Fauth U., Kobayashi T., Huskisson N.S., Barker P.J.,
                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
1,4-BETA-D-GLUCANOHYDROLASE (EC 3.2.1.4) (FRAGMENT).
Clostridium thermocellum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLONE XP15H8B) (FRAGMENT).

(Mono sapidons (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                 Demain A.L.; "Purification and characterization of a new endoglucanase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13; DB 4; Length 8; Pred. No. 3.7e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RBCL PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                       C2C1AB1DD9D1B775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        26.5%; Score 13; DB 2; 1 66.7%; Pred. No. 3.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                  PRT;
                                                                                                                                                                                                                               MEDLINE=92231850; PubMed=1567379;
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66.7%;
                                                                                                                                                                                                                                                                                                  Clostridium thermocellum.";
Biochem, J. 283:69-73(1992)
SEQUENCE 8 AA; 823 MW; (
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Hum. Mol. Genet. 0:0-0(0).
EMBL; L32070; AAA73879.1;
NON_TER 1 1
NON_TER 8
SEQUENCE 8 AA; 865 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                  PRELIMINARY;
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Matches 2; Conserv
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SEQUENCE FROM N.A.
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Best Local Similarity
                                                                                                                                                                           NCBI_TaxID=1515;
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                                                                                                                                                             Clostridium
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1 SPT 3
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                  09R5L7
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Q15889
09R5L7
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BEALT T.M., Kinscherf T.G., Uchytil T.F., Willis D.K.;

Barta T.M., Kinscherf T.G., Uchytil T.F., Willis D.K.;

Box sequence and transcriptional analysis of the tblA gene required for tabtoxin blosynthesis by Pseudomonas syringae.";

Appl. Environ. Microbiol. 59:458-466(1993).

EMBL; S54909; AAR25381.2;
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STRAIN-BC-PLA 9316, AND BC-PLA 9303;
Bard S.J., Handley B.A., Hayes P.K., Walsby A.E.;
"The diversity of gas vesicle genes in Planktothrix rubescens from Lake Zurich.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                            Pseudomonas syringae.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last amoration update)
RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYCENASE LARGE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.6%; Score 14; DB 2; Length 9; 33.3%; Pred. No. 3.7e+05; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.5%; Score 13; DB 2; Length 8; 66.7%; Pred. No. 3.7e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix
NCBI_TaxID=59512;
                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 9 9 9 SEQUENCE 9 AA; 1037 MW; 2B34D9D5BB05B047 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA; 957 MW; 33D1AAA685BB19CB CRC64;
                                                                   9 AA.
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                                                                                                                                                         HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
                                                                                                      Created)
                                                                   PRT;
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EMBL; AJ132249; CAB59537.1; -
EMBL; AJ132248; CAB59534.1; -
NON_TER 1 1
SEQUENCE 8 AA; 957 WW; 33D1AZ
                                                                                                01-FEB-1997 (TrEMBLrel. 02, 01-JAN-1998 (TrEMBLrel. 05, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 33.3
Matches 2; Conservative
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                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
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Matches 2; Conserv
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2 PISESF 7
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EFE 3
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                               RESULT 10
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Q9R3X0
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                         chioroplast.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Cucurbitales; Begoniaceae; Begonia.
NCBI_TaxID=80370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Begoniaceae; Begonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence announcement: rbcL promotor gene in Begonia formosana.";
"Sequence announcement: rbcL promotor gene in Begonia formosana.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009602; CAB52129-1;
EMBL; AJ009601; CAB52127.1;
-...
EMBL; AJ009601; CAB52127.1;
-...
EMBL; AJ009601; CAB52127.1;
-...
EMBL; AJ009601; CAB52127.1;
-...
BND_TER 8
SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;
                                                                                                               SEQUENCE FROM N.A.
Chiang T.Y.;
"Sequence announcement: rbcL promotor gene in Begonia formosana.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009597; CAB52119.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
26.5%; Score 13; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RBCL PROTEIN (FRAGMENT).
                                                                                                                                                                                                     8 AA.
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Best Local Similarity 66./",
"Thes 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Begonia taipeiensis,
               Begonia formosana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chiang T.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast.
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1 MSP 3
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1 MSP 3
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Q9T2Y2
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Search completed: January 17, 2001, 13:44:41 Job time: 195 sec

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Perfect score:

Sequence:

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Searched:

Database

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Sequence 19, Appl
Sequence 3, Appli
Sequence 24, Appl
Patent No. 5179007
Patent No. 5194592
                                                                                                                                                                                          Sequence 54, Apr. Sequence 54, Apr. Sequence 170, Apr. Sequence 170, App. Sequence 170, App. Sequence 14, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 25, Appl.
                    Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 462, Application US/08637759B
sequence 462, Application US/0863759B
sequence 500
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS: 501
CORRESPONDENCE ADDRESS: 501
CORRESPONDE PATECAL. Pabst
STREET: 2800 One Atlantic Center
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COMPUTRY: USA
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Pred. No. 1.3e+05;
1; Mismatches 0;
                  US-08-462-018-24
US-08-812-245-24
US-08-687-956A-19
PCT-US91-03388-3
PCT-US92-09443A-24
5179007-7
                                                                                                                                                                                          US-07-958-903A-54
US-08-462-018-54
US-08-189-331-170
US-08-823-245-54
US-08-433-7380-43
PCT-US92-09443A-54
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US-07-958-903A-25
JS-07-800-364B-3
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Matches 4; Conserv
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Sequence 9, Appli
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Sequence 462, App
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Sequence 23, Al
Sequence 23, Al
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Sequence 39, Sequence 40, Sequence 41, Sequence 42, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 17, Sequence
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Sequence 20,
Sequence 27,
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Patent No. 521
Patent No. 525
Patent No. 546
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Sequence 24,
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/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-075-257A-9
US-08-464-355-5-5
US-08-464-355-5-3
US-08-318-856A-3
US-08-335-733D-39
US-08-335-733D-41
US-08-335-733D-41
US-08-335-733D-41
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US-08-344-831B-27
PCT-US9-02121-17
US-08-44-831B-27
US-08-44-831B-27
US-08-918-856A-20
US-08-918-856A-27
US-08-924-695A-49
5210029-5
5256769-4
5256769-4
US-08-318-856A-7
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US-08-318-856A-7
US-08-318-856A-7
US-08-318-856A-10
US-08-318-856A-10
US-08-318-856A-10
US-08-918-95A-49
US-08-918-918-918-41
US-08-918-918-918-41
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US-08-871-355A-462
5194592-48
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                                                                                                                                                                   January 17, 2001, 13:42:56
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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49
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Score

Result

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APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
OORRESPONDENCE ANDRESSE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.3e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALF: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PCC comparible
OPERATING SYSTEM: PCCDOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/18,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
RICH APPLICATION NUMBER: AB 92 08 058.8
FILING DATE: AUGUST 3, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%; Score 23; DB 2; 1
66.7%; Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Plasmodium falciparum US-08-318-856A-4
                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08318856A Patent No. 5972351 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 8 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
APPLICATION NUMBER: 136,647 FILING DATE: 22-DEC-1987
                                                                                                                                               46.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFERMATION FOR SEG ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             Query Match 46.9
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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                                                            LENGTH: 7
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US-08-318-856A-4
                                           ; SEQ ID NO:48:
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                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 30309-3450
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 1-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Patent No. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
; POLYPEPTIDES DERIVITIVES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
                                                                                                                US-08-871-355A-462
Sequence 462, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8794
INFORMATION FOR SEC ID NO: 462:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 83
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/318,527
FILING DATE: 3-MAR-1989
PRIOR APPLICATION DATA:
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80.0%;
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NO
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Best Local Similarity
'The 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; HYPOTHETICAL:
US-08-871-355A-462
                     ||:||
1 KDDFD 5
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1 KDDED 5
5 KDEFD 9
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5194592-48
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APPLICANT: HOSHING, FUMILIKO
APPLICANT: HIRAI, MASANA
APPLICANT: HIRAI, MASANA
APPLICANT: HIRAI, MASANA
APPLICANT: SATING, FUTTONU
APPLICANT: SARAI, KIYOKO
APPLICANT: SARAI, KIYOKO
APPLICANT: SOLYPEPTIDE POSSESSING PROTEIN DISULIPILI;
TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR TITLE OF INVENTION: PRODUCING THE SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: ADDRESSE: ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                     ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.9%; Score 22; DB 1; Let 80.0%; Pred. No. 1.3e+05; ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION 1935

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-135254

FILING DATE: 27-MAY-1992

PRIOR APPLICATION NUMBER: JP 5-44013

FILING DATE: 04-MAR-1993

PRIOR APPLICATION NUMBER: JP 5-44014

FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5496719man F.

REGISTRATION NUMBER: 2, 618

REGISTRATION NUMBER: 2, 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68-228-0
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Patent No. 5700659
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APPLICANT: YAMADA, YUKIO
APPLICANT: ASAMI, OSAMU
APPLICANT: SUGIYAMA, HIDEHIKO
APPLICANT: IDEKOBA, CHIE
                      SUGIYAMA, HIDEHIKO IDEKOBA, CHIE HOSHINO, FUMIHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24855 OPAT UR
INFORMATION FOR EGO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 6
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Best Local Similarity 80.0
Matches 4; Conservative
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FILING DATE: 19930527
      OSAMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia COUNTRY: U.S.A.
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| KDTFD 5
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                                                                                                                        US-09-075-257A-9

Sequence 9, Application US/09075257A

Patent No. 6074645

GENERAL INFORMATION:
APPLICANT: DIAMOND, DON JEFFREY
APPLICANT: YORK, JOANNE
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES
TITLE OF INVENTION: OF HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,257A
FILING DATE: 11-MAY-1998
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 09/021,298
FILING DATE: 10-FEB-1998
PRIOR APPLICATION NUMBER: US 08/950,064
FILING BAPLICATION DATA:
APPLICATION NUMBER: US 08/950,064
FILING DATE: 14-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/950,4064
FILING DATE: 12-OVY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/747,488
FILING DATE: 12-NOY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                     E: BART G. NEWLAND
555 13TH STREET, NW SUITE 701E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1954-112CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08068395A Patent No. 5496719 GENERAL IMPORMATION: GENERAL TREORMATION: APPLICANT: YAMADA, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NEWLAND, BART G
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-783-60.
TELEFAX: 202-783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                              WASHINGTON
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
  4 TKDEFD 9
                           : | | | | | 2 SKDELD 7
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 PTKD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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Gaps
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              COLLAGEN-INDUCED PLATELET AGGREGATION
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                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/462,894
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,185
FILING DATE: 07-MAR-1994
APPLICATION NUMBER: US 08/116,889
FILING DATE: 07-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/02052
FILING DATE: 04-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,383
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,883
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,884
FILING DATE: 31-DEC-1991
PRIOR APPLICATION NUMBER: US 07/814,884
FILING DATE: 31-DEC-1991
PRIOR APPLICATION NUMBER: US 07/756,211
FILING DATE: 03-SEP-1991
ATPONEY/AGENT INPORMATION:
AMARE: UNIVERSATION DATA:
AMARE:
                                                                                                                       ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOESKE-JUNGBLUT, CHRISTIANE
HAENDLER, BERNHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCH 1359
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Patent No. 5756454
GENERAL INFORMATION:
APPLICANT: HAENDLER, BERNHARD
APPLICANT: KRAFTZSCHARK, JOERN
APPLICANT: SCHLEUNING, WOLE-DIETER
APPLICANT: ALAGON, ALEJANDRO
APPLICANT: ALAGON, ALEJANDRO
APPLICANT: POSSANI, LOURIVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRAETZSCHMAR, JOERN
SCHLEUNING, WOLF-DIETER
ALAGON, ALEJANDEO
POSSANI, LOURIVAL
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: HAMLET-KING, DIANA REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 57.17
احد 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-243-6410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
           TITLE OF INVENTION: CONTILLE OF INVENTION: INVINUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-462-894-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                           STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PTKDEFD 9
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US-08-206-185-23
                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                              POLYPEPTIDE POSSESSING PROTEIN DISULFIDE ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR PRODUCING THE SAME
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                                                                                                           APPLICANT: INTELY, KIYOKO
APPLICANT: SARAI, KIYOKO
TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE
TITLE OF INVENTION: PRODUCING THE SAME
TITLE OF INVENTION: PRODUCING THE SAME
TITLE OF INVENTION: PRODUCING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlinginia
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 1; Length 8; Pred. No. 1.3e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202

ZIP: 22202

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIECCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-135254
FILING DATE: 27-WAY-1992
PRIOR APPLICATION NUMBER: JP 5-44013
FILING DATE: 04-WAR-1993
PRIOR APPLICATION NUMBER: JP 5-44014
FILING DATE: 04-WAR-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Oblon, NO. 5700659man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 68-228-0
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOESKE-JUNGBLUT, CHRISTIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAENDLER, BERNHARD
KRAETZSCHMAR, JOERN
SCHLEUNING, WOLF-DIETER
ALAGON, ALEJANDRO
POSSANI, LOURIVAL
CUEVAS-AGUIRRE, DELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/08462894
Patent No. 5723312
GENERAL INFORMATION:
APPLICANT: NOESKE-JUNGBLUT, CHRIS
APPLICANT: HAENDER, BERNHARD
APPLICANT: HAENDER, SERNHARD
APPLICANT: SCHLEUNING, WOLF-DIETE
HOSHINO, FUMIHIKO
HIRAI, MASANA
KAJINO, TSUTOMU
IMAEDA, TAKAO
SARAI, KIYOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.98;
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(703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248855 OPT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-464-365-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
TELEFAX: (
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| KDTFD 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-462-894-23
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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Score 22; DB 2; Length 8;
Pred. No. 1.3e+05;
0; Mismatches 1; Indels
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APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HILA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 Rockefeller Plaza
                                                                                       ZIP: 20006
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION NUMBER: US/08/318,856A
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION NUMBER: WO PCT/GB93/00731
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PPIR1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-820
TELEPRAX: (202) 721-820
INFORMATION FOR SEQ ID NO: 3:
  STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08335733D Patent No. 6042831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 8 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                          Washington
                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KDEFD 9
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                                             STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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Sequence 3. Application US/08318856A

Patent No. 5972351

GENERAL INFORMATION:

APPLICANT: Adrian V.S. Hill, et al.

TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-

TITLE OF INVENTION: RESTRICTED CTL RPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE

TITLE OF INVENTION: ANTIGENS (AS AMENDED)

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
              TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION TITLE OF INVENTION: INHIBITOR NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 1; Length 8; Pred. No. 1.3e+05; 0; Mismatches 3; Indels
                                                                                            ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD., SUITE 1400
STATE: VIRGINIA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,185 FILING DATE: 0'-MAR-1994 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wenderoth, Lind & Ponack, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION UNBER: US 08/116,889
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,383
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,884
FILING DATE: 31-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,884
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCH 1359
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CUEVAS-AGUIRRE, DELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,302
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-206-185-23
                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: MILLEN, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/08335733D
Patent No. 6042831
GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90
CORRESPEDNDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.5%; Score 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESO VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILIG DATE: 10-NOV-1994
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MacLeod, Janet M
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                            44.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                     FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-335-733D-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 212-408-25(TELEFAX: 212-765-2519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>8</u>
                                                                                                      HYPOTHETICAL: N
ANTI-SENSE: NO
                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                   1 MAPTK 5
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-335-733D-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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Pred. No. 1.3e+05;
1; Mismatches 0; Indels
                                                                                                  NAME: MacLeod, Janet M
REGISTRATION NUMBER: 35,263
REGISTRATION NUMBER: A29928-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MacLeod, Janet M
REGISTRATION NUMBER: 35,263
REFRENCE/DOCKET NUMBER: A299
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 40:
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80.0%;
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FILING DATE: 10-NOV-1994
                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 44.9°
Best Local Similarity 80.0°
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                              ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-335-733D-39
                                                                                                                                                                                        TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps
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                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYEE FLORPY disk
COMPUTER: FLORPY disk
COMPUTER: IBW PC COMPALIBLE
COMPUTER: MINDOWS NT
SOFTWARE: ASCII DOS TEXT
SOFTWARE: ASCII DOS TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,776C
FILING DATE: 04-JAN-1996
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
FILING DATE: 06-JAN-1995
APPLICATION NUMBER: US 08/43,831
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: COLNICALIL, MATGARET A.
RECISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279-194C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: January 17, 2001, 13:42:57 Job time: 156 sec
                                                         Schneider, Patrick A.
Stitz, Lothar
              Briese, Thomas
Kliche, Stefanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SECTIONO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213/680-4518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: USA
21P: 90017-2576
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APPLICANT:
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US-08-335-733D-42
Sequence 42, Application US/08335733D
Fatent No. 6042831
GENERAL INFORMATION:
TATLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 30 Rockefeller Plaza
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%; Score 22; DB 3; Length 8; 80.0%; Pred. No. 1.3e+05;
Pred. No. 1.3e+05;
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                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-582-776C-27
Sequence 27, Application US/08582776C
Setact No. 6077510
GENERAL INFORMATION:
APPLICANT: Lipkin, W. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MacLeod, Janet M
REGIESTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: AZ
TELECOMMUNICATION INFORMATION:
              80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
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TELEFAX: 212-765-2519
              Best Local Similarity 80.0 Matches 4; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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STATE: NY
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Cadherin-7 cell

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                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268485 seqs, 34193795 residues
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                                                                                                                                                                                   January 17, 2001, 13:42:22
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Listing first 45 summaries
                                                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 ENMERNCRA 9
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Match 1
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Maximum DB
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Factor VIII antige HRE-I affinity pep Membrane dipeptida HLA-B8-binding HIV Cadherin-7 cell ad Cadherin-14 cell a Cadherin-related n W30412 Y48654 Y66247 Y61508 Y62238 Y64309 R90952 18 20 21 21 21 21 21 21 21 21

Amino acid sequenc Cadherin-7 cell ad Cadherin-14 cell a Cadherin-related n Human leucocyte an

P93523 Y61511 Y62239 Y64312 W49414

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Y48654 standard; Peptide; 9 AA.
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Y48654
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       Peptides R90945-64 are derived from the factor VIII protein, esp. from a modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to von Willebrand factor, esp. antibodies, thus preventing or treating immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               target genes. The plasmid comprises a sequence encoding the test peptide, a promoter comprising the target gene, and a reporter gene bound to the promoter. The present sequence represents a specifically claimed peptide with affinity to HRE-I. The plasmids are used for screening for peptides which bind to target genes. The identified peptides can be used for the treatment of conditions associated with the inhibition of the expression the genes, and treatment of conditions
                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                       Binding site; HRE-I; screening; H-Ras; target gene; plasmid; inhibition; affinity peptide.
                                                                                                                   Length 9;
                                                                                                                                       Indels
                                                                                                                  100.0%; Score 50; DB 17;
100.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  HRE-I affinity peptide SEQ ID NO:30.
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                                                                                                                                                                                                                                    W30412 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         96JP-0263345.
96JP-0101990.
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                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated with H-Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-503115/46
                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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(YAWA ) NIPPON
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01-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                    Sequence
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                                                                                        Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides which selectively home to organs or tissues, used se.g. identifying target ligands and for therapy of pathological conditions
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Pred. No. 2.1e+05;
3; Mismatches 1; Indels
                                             Membrane dipeptidase-binding lung homing peptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruoslahti EI;
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                                                                                                                                                                                                                                                                                                                                                                                                                98US-0042107
                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0042107
10-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rajotte D, Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-571717/48
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
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qdirrnc 9
                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                    WO9946284-A2.
                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1999;
                                                                                                                                                                                                                                                                                                                  16-SEP-1999
                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Gaps

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Indels

Length 7;

DB 18; L 2.1e+05; ö

Query Match 50.0%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 2.1 Matches 4; Conservative 0; Mismatches

02-MAR-2000 (first entry)

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Novel methods for designing molecular conjugate therapeutics which are used for diagnosis, imaging and treatment against pathogens
                 human leukocyte antigen; allele; binding; conserved; genome; peptide; trargetting; toxio; drug; antibody; antigen; antiviral; molecular conjugate therapeutic; diagnosis; treatment; pathogen; localisation; quantification; detection; infection; drug resistance;
         HIV-1; MHC; major histocompatibility complex; Class I; HLA;
                                                                                                                                                                                  Weng Z,
                                                                                                                                                                                  Gulukota K, Vaccaro D,
                                                                      Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                               Example 3; Page 46; 62pp; English.
                                                                                                                           99WO-US07111.
                                                                                                                                             98US-0052530.
                                                                                                                                                                                  Berzofsky J,
                                                                                                                                                              (UYBO-) UNIV BOSTON.
                                                                                                                                                                                                  WPI; 2000-038361/03
                                                     immune response
                                                                                        WO9949893-A1.
                                                                                                                           31-MAR-1999;
                                                                                                                                             31-MAR-1998;
                                                                                                          07-0CT-1999
                                                                                                                                                                                 Delisi C,
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Ye6199-Ye6413 are peptides derived from conserved portions of the HIV-1 genome which bind to different HLA alleles of MHC (major histocompatibility complex) class I molecules. The peptides are used to construct targetting antiqens compiration one or more peptides bound to the corresponding MHC class I molecule, which can be used to raise antibodies. The antibody may then be used as a targetting vehicle to deliver a potentially toxic drug to its target site of action, rather than administering it systemically, which may result in adverse side effects. The invention relates to improved methods for the deasign of molecular conjugate therapeutics for the diagnosis and treatment of infections caused by pathogens with a high mutation rate (such as HIV-1). This method involves identifying conserved peptide-encoding regions among the genomes of multiple variants of a pathogen, identifying the Class I MHC molecules which occur with greatest frequency in a population of interest (e.g., human sub-populations), and determining which of the corresponding class I MHC molecules. The MHC-binding peptides and the corresponding antigens, which are in turn used to produce the corresponding antigens, which are in turn used to produce targetting antibodies. The methods may be used in localisation, quantification and in situ detection of specific peptide-MHC Class I complexes and also to detect and treat viral infection. The methods of the invention mitigate against the development of viral resistance to drugs and to the immune response, as well as providing a solution for targetting toxic compounds to destroy viruses sequestered in sites not accessible to T cells. In addition, the methods eliminate the virus, whereas current therapies only arrest viral replication. Sequence

ö Gaps ö Length 9; Indels DB 21; Ld 2.le+05; hes 0; Mismatches NO. Score 24; Pred. No. 48.0%; Scur 100.0%; Pre 0; ! Query Match 48.0 Best Local Similarity 100. Matches 4; Conservative

X61508

Y61508 standard; Peptide; 7 AA.

Y61508; AX S

||||| | ncra 4 NCRA 9 RESULT g

inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin; cadherin; cadherin; cadherin; cadherin; cadherin; cadherin; camoulin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic. Cadherin-7 cell adhesion recognition cyclic pept1de SEQ ID NO:1394. nonclassical cadherin mediated cell adhesion; CAR; Location/Qualifiers 1..7 98US-0187859. 99US-0234395. 99US-0264516. 99WO-CA00363 98US-0073040 Disulfide-bond W09957149-A2. Homo sapiens. 05-MAY-1999; 08-MAR-1999; 11-NOV-1999 05-MAY-1998 06-NOV-1998 20-JAN-1999 Synthetic

Zhang C;

New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease

(ADHE-) ADHEREX TECHNOLOGIES INC.

Gour BJ, Byers S;

Blaschuk OW,

WPI; 2000-038791/03

Claim 36; Page 172; 252pp; English.

comprising peptides which comprises cancerin modulating of an operation describes cancerin modulating cancering peptides which comprises a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAS can be used for modulating nonclassical cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug through the skin of a mammal, canamoing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, stimulating angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherincexpressing cell, preventing or treating obesity in a mammal, stimulating central nervous system, treating a demylating drug delivery to the central nervous system, treating a demylating adhesion of increasing vasopermeability in a mammal, enhancing adhesion of conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing e.g. e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. Y60592 to Y64572 represent specifically claimed peptides, and X64573 to Y64643 and 233183 to 233186 represent sequences used in the The present invention describes cadherin modulating agents (MA) exemplification of the present invention.

7 AA; Seguence

Score 23; DB 21; Pred. No. 2.1e+05; 46.0%; Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes cadherin modulating agents (MA) comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The Mas can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating aneatasis of a cancer in a mammal, inhibiting metactasis of a poptosis in a nonclassical cadherin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressing cell, preventing or treating obesity in a mammal, stimulating
                                                                                                                                                                                                                                                                                                                cadherin extracellular domain; cell adhesion recognition;
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                              Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3973.
                                                                                                                                                                                                                                                                                                                               OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin; related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmocollin; calclum binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
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                                                                                                                                                                                                                                                                                                  nonclassical cadherin mediated cell adhesion; CAR;
   Indels
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   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADHE-) ADHEREX TECHNOLOGIES INC.
 5;
                                                                                                                                                       Y62238 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0073040.
98US-0187859.
99US-0234395.
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                                                                                                                                                                                                                             (first entry)
 Conservative
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                                  NMERNC 7
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20-JAN-1999;
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                                                                                                                                                                                                                                                                                                Modulation;
                                                                                                                                                                                                                                                                                                                  inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1998;
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3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                           Y62238;
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mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. Y60592 to Y64572 represent specifically claimed peptides, and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin, cadherin-5; cadherin-6; cadherin-7; cadherin-18; cadherin-12; cadherin-13; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoolin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                             0;
                                                                                                                                                                           Length 7;
                                                                                                                                                                                                             1; Indels
                                                                                                                                                                         Score 23; DB 21;
Pred. No. 2.1e+05;
                                                                                                                                                                                                           2; Mismatches
                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 102; Page 217; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Byers S;
                                                                                                                                                                                                                                                                                                                                                                Y64309 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0187859.
99US-0234395.
99US-0264516.
                                                                                                                                                                         46.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-038791/03.
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                          7 AA;
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2 nidanc
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20-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                           Seguence
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Caps

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Length

Score 23; DB 10; Lv Pred. No. 2.1e+05; 0; Mismatches 3;

46.0%; 62.5%;

5; Conservative

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Query Match Best Local Similarity Matches 5; Conserv

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cc mammal, enhancing delivery of a drug through the skin of a mammal, contanting delivery of a drug to a tumour in a mammal, inhibiting a mammal, inhibiting and anammal, inhibiting and anglogenesis in a mammal, inhibiting and anglogenesis in a mammal, inhibiting anglogenesis in a mammal, inhibiting anglogenesis in a mammal, inhortang anglogenesis in a mammal, inhibiting anglogenesis in a mammal, inhibiting admission in a mammal, inhancing delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of central nervous system, in a mammal, enhancing adhesion of a mammal, or preventing pregnancy in a mammal. They can also be used for cey. enhancing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in proceeding to the present sequences used in the central and y64573 to 233186 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Matches
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2 NMERNC 7 |:: || 2 nidsnc 7 ò g

Amino acid sequence of polylinker region of transfer vector pBF133. Polyhedrin protein; silkworm nuclear polyhedrosis virus; NPV; HIV gene; gag; pol; SOR; gp120; gp41; polylinker region; pBF133. P93523 standard; protein; 8 AA. 03-JUN-1990 (first entry) P93523; P93523

87JP-0231107 JP01074990-A. 17-SEP-1987; 20-MAR-1989

(MAED) MAEDA S.

87JP-0231107

17-SEP-1987;

WPI; 1989-127530/17. N-PSDB: N92399 New transfer vector pBFs, for HIV diagnosis -contg. promoter region of polyhedrin protein gene for slik-worm nuclear polyhedrosis virus deoxyribonucleic acid

Fig 2; page 9; 11pp; Japanese.

Transfer vectors pBFs were prepd. contg. promoter region of polyhedrin protein gene of silkworm nuclear polyhedrosis virus (NPV) recombined with HIV gene gag, pol, SOR, gpl20 or gp41 in the polylinker region of the vector. Thus, HIV antigenic protein can be produced in large amts. and used as an antigen for the diagnosis of HIV or for vaccine production.

8 AA; Sequence

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comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anglogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
expressing cell, preventing or treating obesity in a mammal, stimulating
blood vessel regression in a mammal, enhancing drug delivery to the
central nervous system, treating a demyelinating neurological diseasc,
increasing vasopermeability in a mammal, enhancing adhesion of
nonclassical cadherin-expressing cells, inhibiting synaptic stability in
a mammal, or preventing pregnancy in a mammal. They can also be used for
                                                                                                                                                                                  Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-12; cadherin-12; cadherin; PB-co-iherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoolin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                   Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes cadherin modulating agents (MA)
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 1..8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 36; Page 172; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ADHE-) ADHEREX TECHNOLOGIES INC.
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                                   Y61511 standard; Peptide; 8 AA.
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98US-0187859.
99US-0234395.
99US-0264516.
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                                                                                                           02-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                        Y61511;
6
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e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bloreactors. v60592 to v64572 represent specifically claimed peptides, and X64573 to x64573 represent specifically claimed peptides, and X64573 to x64643 and 233186 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin-7; cadherin-8; cadherin-17; cadherin-8; cadherin-12; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoclalin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3974
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 8; 2.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 2
Pred. No. 2.1e<sup>4</sup>
2; Mismatches
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99US-0234395.
99US-0264516.
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                              8 AA;
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08-MAR-1999;
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                                                                                                                                                                                                                                                                                                 Sequence
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expressing cell, preventing or treating obesity in a mammal, stimulating
blood vessel regression in a mammal, enhancing drug delivery to the
central nervous system, treating a demyelinating neurological disease,
increasing vasopermeability in a mammal, enhancing adhesion of
nonclassical cadherin-expressing cells, inhibiting synaptic stability in
a mammal, or preventing pregnancy in a mammal. They can also be used for
or reducing scar tissue, or enhancing adhesion of foreign tissue in
mammal. They can also be used for treating e.g. psoriasis, arthritis,
age-related macular degeneration, multiple sclerosis and diabetes. The
products can also be used for treating e.g. psoriasis, arthritis,
products can also be used for treating end diabetes. The
products can also be used for treating end diabetes. The
products can also be used for and diaposis and in
bioreactors. Y60592 to Y64572 represent specifically claimed peptides,
and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
              inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin, cadherin-5; cadherin-6; cadherin-7; cadherin, B$; cadherin-12; cadherin, PB-cadherin; pB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmoglein; calclum binding; cancer; tumour; obesity; neurological disease; cyclic.
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Pred. No. 2.1e+05;
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                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention
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98US-0187859.
99US-0234395.
99US-0264516.
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Best Local Similarity
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20-JAN-1999;
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the treatment of auto:immune disease
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                                                                                                                                                                                                                                                                                                                                                                                               a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, agerelated macular degeneration, multiple sclerosis and diabetes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     products can also be used for detection and diagnosis and in
bioreactors. Y60592 to Y64572 represent specifically claimed peptides,
and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
                                                                                                                                                                                                                     inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting apoptosis in a monclassical cadherinexpressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in
                                                                                                                                                  The present invention describes cadherin modulating agents (WA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                              New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human leucocyte antigen DQ4 binding peptide #305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention.
                                                                                                                    Claim 102; Page 217; 252pp; English
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WPI; 2000-038791/03
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W49414
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HLA-binding oligopeptide and an immuno: regulator contg it - used in

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                               This peptide is an example of a peptide which binds to a human leucocyte entigen HLA-DQ4 molecule. The peptide was isolated from a phagemid combinatorial library comprising the sequence V05953, by screening with an HLA-DQ4 molecule. The peptide is used for the treatment of autolmmune disease, or especially for treatment of viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-13; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglain; desmoclalin; calcium binding; cancer; tumour; obesity; rhemmatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                       Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1400
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                                                                                                                                                                                   Score 23; DB 17; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                    Length 9;
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Claim 4; Page 37; 61pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                         Y61514 standard; Peptide; 9 AA.
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80.0%;
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99US-0234395
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Best Local Similarity
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3 rrcra 7
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20-JAN-1999;
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                                                                                                                                       Seguence
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conclassical cadherin-mediated functions. They can be used for e.g.
inhibiting adhesion of nonclassical-cadherin expressing cells in a
monaclassical cadherin-mediated functions. They can be used for e.g.
inhibiting adhesion of nonclassical-cadherin expressing cells in a
comman, enhancing delivery of a drug through the skin of a mammal,
comman, inhibiting metastasis of a cancer in a mammal, inhibiting
angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
compressing cell, preventing or treating obesity in a mammal, stimulating
contral nervous system, treating a demyelinating neurological disease,
contral nervous system, treating a demyelinating neurological disease,
contral nervous system, in a mammal, enhancing adhesion of
conclassical cadherin-expressing cells, inhibiting synaptic stability in
a mammal, or preventing pregnancy in a mammal. They can also be used for
cor reducing scar tissue, or enhancing adhesion of foreign tissue in a
cor reducing scar tissue, or enhancing adhesion of foreign tissue in a
cor reducing scar tissue, or enhancing adhesion of foreign tissue in a
cor reducing scar tissue, or edection and diagnosis and in
cor mammal. They can also be used for treating e.g. psociasis, arthritis,
age-related macular degeneration, multiple sclerosis and diabetes. The
cor products can also be used for teating e.g. psociasis, arthritis,
and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
correctors. Y60592 to Y64572 represent specifically claimed peptides,
and Y64573 to Y64643 and 233186 represent sequences used in the
correctors.
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recognition (CAR) sequence. The MAs can be used for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.0%; Score 23; DB 21; Length 9; 50.0%; Pred. No. 2.18+05; Live 2; Mismatches 1; Indels
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99US-0264516.
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Gour BJ, Byers S;

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The present invention describes cadherin modulating agents (WA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, chancing delivery of a drug to a tumour in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting confidences in a monclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing adusion of increasing vasopermeability in a mammal, enhancing adhesion of increasing vasopermeability in a mammal, enhancing adhesion of conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing cels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   products can also be used for detection and diagnosis and in
bioreactors. Y60592 to Y64572 represent specifically claimed peptides,
and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-6; cadherin-7; cadherin-18; cadherin-12; cadherin-12; cadherin-15; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmocplin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                            New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention.
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                                                                                                                                                                     Claim 54; Page 184; 252pp; English.
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Disulfide-bond
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The present invention describes cadherin modulating agents (MA)

comprising peptides which comprise a nonclassical cadherin cell adhesion

crecognition (CFAR) sequence. The MAs can be used for modulating

nonclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a

mammal, enhancing delivery of a drug through the skin of a mammal,

can mammal, inhibiting metastasis of a cancer in a mammal, inhibiting

angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-

expressing call, preventing or treating obesity in a mammal, stimulating

blood vessel regression in a mammal, enhancing delivery to the

central nervous system, treating a demyelinating neurological disease,

increasing vasopermeability in a mammal, enhancing adhesion of

conclassical cadherin-expressing cells, inhibiting synaptic stability in

a mammal, or preventing pregnancy in a mammal. They can also be used for

c g. enhancing or directing neurite outgrowth, facilitating wound healing

or reducing scar tissue, or enhancing adhesion of foreign tissue in a

mammal. They can also be used for treating e.g. psoriasis, arthritis,

age-related macular degeneration, multiple sclerosis and diabetes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   products can also be used for detection and diagnosis and in
horeactors. V60502 to Y64572 represent specifically claimed peptides,
and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                       New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 102; Page 217; 252pp; English.
                                                                                                                                                                                               (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                         Byers S;
                                                                                                      98US-0187859.
99US-0234395.
99US-0264516.
                                                                                    98US-0073040
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                                                                                                                                                                                                                                         Gour BJ,
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06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
                                                                                                                                                                                                                                       Blaschuk OW,
                                          05-MAY-1999;
11-NOV-11999
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Search completed: January 17, 2001, 13:42:23 Job time: 137 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 17, 2001, 13:43:37 Run on:

; Search time 36.59 Seconds
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16.701 Million cell updates/sec

US-08-765-837-8 50 Perfect score: Title:

1 ENMERNCRA 9 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

195891 segs, 67900655 residues

Searched:

787 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_66:* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	conopressin S - co		oxytocin-related p	lysine-conopressin		MHC H2-K-k cell su	٠	•	•	oxytocin - Austral	oxytocin - rabbit	arginine vasotocin	vasotocin - common	acylaminoacyl-pept	mabinlin II chain	L-serine dehydrata	olfactory receptor	gene Cftr protein	olfactory receptor	isotocin - common	diuretic neuropept	metallothionein is	R-phycoerythrin ga	P element, P cytot	probable minipolyp	T-cell receptor be	hypothetical prote	al	quinoline 2-oxidor
SUMMARIES	TD	B28495	A28495	PC2021	S39040	I57532	I67345	A91466	A92774	A93147	A93408	в90667	806375	B61364	A49792	S38516	A25836	A54823	157018	B54823	A61364	A29477	S59622	A37521	A39892	B45020	PH0921	B44510	PC4127	866608
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æ	Query Match	40.0	40.0	40.0	40.0	34.0	32.0	32.0	32.0					32.0		30.0	30.0	30.0	30.0	30.0	30.0	30.0	28.0	28.0	28.0	28.0	28.0	26.0	26.0	26.0
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cardioactive pepti	cardioactive pepti	cardioactive pepti	synaptosomal-assoc	20K protein · Rick	hemoglobin, extrac	cytotoxic T-lympho	galactose oxidase	formylglycinamide	tumor-associated a	tumor-associated a	leucinetRNA liga	T-cell receptor al	sperm-activating p	gene NF2 protein -	gastrin - domestic
A26363	S27233	S39767	E44823	B31836	S65726	149424	XEYDGD	A12016	S43971	S43972	PC1002	PH0803	S19329	I54379	C60070
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ALIGNMENTS

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Conopressin S - cone shell (Conus striatus)

N.Alternate names: Arg-vasopressin-S

N.Alternate names: Arg-vasopressin-S

N.Alternate striatus (striated cone)

C.Species: Conus striatus (striated cone)

C.Species: Conus striatus (striated cone)

C.Species: Conus striatus (striated cone)

C.Accession: B28495

E.Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Cray, W.R.; C

J. Biol. Chem. 262, 15821-15824, 1987

A.Tile: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from A.Reference number: A92617; MUID:88058932

A.Accession: B28495

A.Accession: B28495

A.Molecule type: protein

A.Residues: 1-9 <CRU>

C.Superfamily: oxytocin-neurophysin

C.Superfamily: oxytocin-neurophysin

C.Keywords: amidated carboxyl end; venom

F:1-6/Disulfide bonds: #status experimental

F:9/Modified site: amidated carboxyl end (Gly) #status experimental
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Best Local Similarity 100.
Matches 3; Conservative
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4 RNC 6 5 RNC 7 δ q

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Naternate names: Lys-conopressin.G
N;Alternate names: Lys-conopressin.G
S;Special Conus geographus)
N;Alternate names: Lys-conopressin.G
C;Specias: Conus geographus cone)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 25-Apr-1997
C;Accession: A28495
R;Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zelkus, R.; Gray, W.R.; O
A;Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides fro A;Reference number: A92617; MUID:88058932
A;Accession: A28495
A;Molecule type: protein
A;Residues: 1-9 cCRU>
C;Superfamily: oxytocin-neurophysin
C;Superfamily: oxytocin-neurophysin
C;Superfamily: oxytocin-neurophysin
F;1-6/Disulfide bonds: #status experimental
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Gaps ; Query Match 40.0%; Score 20; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 3; Conservative 0; Mismatches 0; Indels

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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Dates: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 167345
EMBO J. 5, 957-965, 1986
A;Title: A single nucleotide difference at the 3' end of an intron causes differentia A;Refcerence number: 153243; MUID:86247587
A;Accession: 167345
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C; Genetics:
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66.7%; Pred. No. 2e+05;
live 1; Mismatches
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2e+05;
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Pred. No. 2e+05
2; Mismatches
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75.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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C;Keywords: glycoprotein
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4 VERN 7
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3 DCKA 6
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C;Genetics:
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R; Oumi, T.; Ukena, K.; Matsushima, O.; Ikeda, T.; Fujita, T.; Minakata, H.; Nomoto, K.
Biochem. Biophys. Res. Commun. 198, 393-399, 1994
A;Title: Annetocin: an oxytocin-related peptide isolated from the earthworm, Eisenia for A;Reference number: PC2021; MUID:94121660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-9 < CUM>
C; Comment: This protein potentiates spontaneous contractions of the gut and also pulsate
C; Keywords: amidated carboxyl end
F;1-6/Disulfide bonds: #status experimental
F;9/Modified site: amidated carboxyl end (Gly) #status experimental
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Eur. J. Blochem. 217, 897-903, 1993

Eur. J. Blochem. 217, 897-903, 1993

A;Title: Isolation, structural characterization and biological function of a lysine-cond A;Reference number: S39040; MUID:94039146

A;Accession: S39040
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C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C; Accession: 157325
R; Banerjee-Basu, S.; Buonanno, A.
Mol. Cell. Biol. 13, 7019-7028, 1993
A; Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and develop A; Reference number: 157532; MUID:94019373
A; Accession: 157532
A; Acces
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C;Species: Erpobdella octoculata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Eisenia foetida (common brandling worm, common dung-worm)
C;Date: 03-May-1994 #sequence_revision 15-Oct-1994 #text_change 11-Jul-1997
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Best Local Similarity 100.
Matches 3; Conservative
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A;Reference number: A93408; MUID:73223515
A;Accession: A93408
A;Accession: A93408
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-9 <ACH>
C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.
C;Superfamily: oxytocin-neurophysin
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; hormone; hypothalamus
F;1-6/Disulfide bonds: #status predicted
F;9/Modified site: amidated carboxyl end (Gly) #status predicted
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                                                                                                       N. Chechains: neurophysin 1; oxytocin C. Species: Hydrolagus colliei (spotted_raffish) C. Date: 30 Oct-1992 #sequence_revision 30 Oct-1992 #text_change 20 -Mar-1998 C. Accession: A92774; A01450; B01450 R. Pickering, B.T.; Heller, H. A. Enderind, 45, 597-606, 1969 A. Endeorinol. 45, 597-606, 1969 A. Title: Oxytocin as a neurohypophysial hormone in the holocephalian elasmobranch fish, A. Molecule type: protein A. A. Molecule type: protein A. Molecule type: amidated carboxyl end; hormone; hypothalamus C. Superfamily: oxytocin neurophysin C. Superfamily: oxytocin-neurophysin C. Superfamily: oxytocin-neurophysin C. Superfamily: oxytocin-serioted for the diported family amidated carboxyl end; hormone; hypothalamus F: 1 G. Disulfide bonds: #status predicted F: 9/Modified site: amidated carboxyl end (Gly) #status predicted
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C: Comment: Oxytocin is followed by neurophysin 1 in the precursor. C: Superfamily: oxytocin-neurophysin C: Keywords: amidated carboxyl end; hormone; hypothalamus F: 1-6/Disulfide bonds: #status experimental F: 9/Modified site: amidated carboxyl end (Gly) #status experimental
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C;Species: Tachyglossus aculeatus (Australian echidna)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A93408; A01450; B01450
C;Accession: A93408; A01450; B01426, M.T.
Nature New Biol. 244, 124-126, 1973
A;Title: Neurohypophysial hormones and evolution of tetrapods.
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Pred. No. 2e+05;
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Pred. No. 2e+05;
L; Mismatches
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                                                               xytocin - spotted ratfish
;Alternate names: neurophysin I
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Matches 2; Conserv
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Ny Alternate names: neurophysin I
Ny Alternate names: neurophysin I
Ny Contains: neurophysin 1; oxytocin
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C; Accession: B90667; A01450; B01450
R; Chauvet, J.; Chauvet, M.T.; Acher, R.
Biochimie 53, 1099-1104, 1971
A; Title: Evolution des hormones neurohypophysaires: isolement des principes actils du A; Reference number: A90667; MUID:72215060
A; McGession: B90667
A; Molecule type: protein
A; Residues: 1-9 < CHA>
C; Comment: Oxytocin 1s followed by neurophysin 1 in the precursor.
C; Comment: Oxytocin 1s followed by neurophysin
C; Superfamily: oxytocin-neurophysin
C; Superfamily: oxytocin-neurophysin
C; Seywords: amidated carboxyl end; hormone; hypothalamus
F; 1-6/Disulfide bonds: #status experimental
F; 9/Modified site: amidated carboxyl end (Gly) #status experimental
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C;Species: Petromyzon marinus (sea lamprey)
C;Species: 29-dan-1993 #sequence_revision 29-dan-1993 #text_change 31-Mar-1997
C;Accession: S06375
R;Lane, T.F.; Sower, S.A.; Kawauchi, H.
Gen. Comp. Endocrinol. 70, 152-157, 1988
A;Title: Arginine vasotocin from the pitultary gland of the lamprey (retromyzon marin A;Reference number: S06375; MUID:88225976
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A; Residues: 1-9 <LAN>
C; Residues: anidated carboxyl end; hormone; neuropeptide; pituitary
F; 1-6/Disulfide bonds: #status experimental
F; 9/Modified site: amidated carboxyl end (Gly) #status experimental
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Score 16; DB 2;
Pred. No. 2e+05;
1; Mismatches
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Gaps

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Length 7; 1; Indels

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30.0%; Score 15; DB 2; 40.0%; Pred. No. 2e+05;
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                                                                                 Best Local Similarity 40.0
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2 QRACQ 6
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                                                                                                                                                                                                                                                                                                                     C; Species: Cyprinus Carpio (common carp)
C; Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C; Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C; Accession: B61364
R; Acher, R; Chauvet, J; Chauvet, M.T.; Crepy, D.
Comp. Biochem. Physiol. A 14, 245-254, 1965
A; Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce A; Reference number: A61364
A; Accession: B61364
A; Residues: 1-9 <ACH>
C; Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: A49792
C;Accession: A49792
Anal. Biochem. 199, 45-50, 1991
A;Title: N-terminal sequence analysis of N(alpha)-acetylated proteins after unblocking A;Reference number: A49792; MUD:92222120
A;Accession: A49792
A;Accession: A49792
A;Accession: A49792
A;Accession: A49792
A;Refundary
A;Molecule type: protein
A;Residues: 1-6 <KRI>
C;KRywords: acetylated amino end; hydrolase; omega peptidase
F;1/Modified site: acetylated amino end (Met) #status experimental
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39816
mabinlin II chain A - Yunnan caper (fragments)
C;Species: Capparis masaikai (Yunnan caper)
C;Species: Capparis masaikai (Yunnan caper)
C;Date: 08-Jun-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: 838516
R;Nirasawa, S.; Liu, X.; Nishino, T.; Kurihara, Y.
Biochim. Biophys. Acta 1202, 277-280, 1993
A;Title: Disulfide bridge structure of the heat-stable sweet protein mabinlin II.
A;Reference number: S38516; MUID:94002261
A;Accession: S38516
A;Accession: S38516
A;Accession: Creation mabinlin II.
A;Reference number: A;Refe
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ilarity 66.7%;
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88757 segs, 32294092 residues

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Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	con	P05487 conus stria	P42998 eisenia foe	P80027 octopus vul	P23879 cyprinus ca	2878	000	154 oryctol	6339	2993			P42997 scyliorhinu			O54296 salmonella	P38498 procambarus	P41486 homarus ame	-	P06294 dactylium d	P81886 porphyromon	P24047 stomopneute	P23210 herpes simp				P81010 fusarium so		papio		P19342 theropithec		P34966 cavia porce
SUMMARIES	ID	ž	CONO_CONST	OXYT_EISFO	OXYT_OCTVU	OXYT_CYPCA	OXYT_RABIT	OXYV_SQUAC	ACPH_RABIT	DNF1_LOCMI	ISOT_CYPCA	OXYA_SCYCA	OXYA_SQUAC	OXYF_SCYCA	OXYT_RAJCL	ULAE_HUMAN	RS11_SALTY	FAR2_PROCL	FAR3_HOMAM	CCAP_CARMA	IGAO_DACDE	B44K_PORGI	SAP_STOVA	VP19_HSV1K	FAR1_PROCL	FARB_CALVO	FAR4_HOMAM	FUSS_FUSSO	UPA1_HUMAN	FIBB_PAPAN	FIBB_PAPHA	FIBB_THEGE	FLA2_TREHY	NEUU_CAVPO
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OXYT_BUFRE BIOB_SALTY HTFI_PERAM HTFI_PERAMO NS3_MYCTU UH09_RAT TAL1_PICJA UF02_MOUSE ULAH_HUMAN	ALIGNMENT PRT; 9	# 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	PubMed=3680228; Sox V., Zafaralla G.(. B.M.; pressin/oxytocin hor sy geographus and Cor ::15821-15824(1987).	22286; 12 L.J.; 18 Conus s 700(1988). THE VASOPR	AMIDATION. D4FC276EB4540059 Score 20; DB 1;), Mismato	PRT; luence cotatio
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Biochem. Biophys. Res. Commun. 198:393-399(1994).

-I- FUNCTION: POTENTIATES SPONTANGOUS CONTRACTIONS OF THE GUT AND ALSO PULSATORY CONTRACTIONS OF THE HE GUT AND ALSO NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH NEPHRIDIA. EUNCTION.

-I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

PIR; PC2021; PC2021.
                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eisenia foetida (Common brandling worm) (Common dung-worm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Eisenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
                                    Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D., Gray W.R., Olivera B.M.;

"Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms.";
J. Biol. Chem. 262:15821-15824(1987).
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                                                                                                                                                                                                                                                                                                                        40.0%; Score 20; DB 1; Length 9; 100.0%; Pred. No. 8.9e+04; ive 0; Mismatches 0; Indels
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SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;
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PROSITE; PS00264; NEUROHYPS_HORM; FALSE_NEG
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                        MEDLINE-88058932; PubMed=3680228;
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MEDLINE-94121660; PubMed-8292046;
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INTERPRO; IPR000981; -.
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Best Local Similarity
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P42998;
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Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
"Characterization of neurohypophyseal hormones from a fresh water bony fish, the carp (Cyprinus carpio). Comparison with hormones from sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cypriniae; Cypriniae;
                                                                                                                                                                                                                               "A new peptide of the oxytocin/vasopressin family isolated from nerves of the cephalopod octopus vulgaris.";
Neurosci. Lett. 134.191-194(1992).
                                                                                                               Octopus vulgaris (Octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
Incirrata; Octopodidae; Octopus.
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MEDLINE-88225976; PubMed=3371648;
Lane T.F., Sower S.A., Kawauchil H.;
Arginine vasotocin from the pituitary gland of the lamprey (Petromyzon marinus): isolation and amino acid sequence.";
Gen. Comp. Endocrinol. 70:152-157(1988).
                                                                                                                                                                                                                                                                                                     -:- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. INTERPRO; IPRO00981; -. PFAM; PF00220; hormone4; 1. PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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9 AA; 1072 MW; 17FF476EB45409DB CRC64;
                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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0; Mismatches
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                              PRT;
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                            STANDARD;
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TISSUE=NERVE ENDINGS;
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MOD_RES
SEQUENCE
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                         OXYT_OCTVU P80027;
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4 RNC 6
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FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE UTERUS AND OF THE MAMMARY GLAND.
SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-72128038; PubMed-4622083;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Identification of 2 new neurohypophyseal hormones, valitocin (val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias)...;
C. R. Acad. Sci., D., Sci. Nat. 274:313-316(1972).
INTERPRO: IPR0009981;
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Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
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Pred. No. 8.9e+04;
1; Mismatches 0; Indels
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17F8376EB456D04B CRC64;
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9 AA; 996 MW; 17EDD76EB456D04B CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
Hormone; Amidation.
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Best Local Similarity 66.7%;
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66.7%;
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                                                 -!- SIMILARITY: BELONGS PIR; A91466; A91466. PIR; A91744; A92774. PIR; A93147. PIR; A93408; A72; L5-OCT-90. APPRES APPROS IRPO00991; APPROS APPR
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P43000;
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OXYV_SQUAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculis (Rabbit), Hippopotamus amphibius (Hippopotamus), Balaenoptera physalus (Finback whale) (Common rorqual), Tachyglossus aculeatus aculeatus (Australian echidna), and Hydrolagus colliei (Spotted raffish) (Pacific raffish) Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE-72215060; PubMed-5150741;
Chauvet J., Chauvet M.-T., Acher R.;
Evolution of neurohypophyseal hormones: isolation of active principles from rabbits and rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=H.COLLIEI;
MEDLINE=70088110; PubMed=5366118;
Pickering B.T., Heller H.;
"Oxytocin as a neurophyophysial hormone in the holocephalian elasmobranch fish, Hydrolaqus collei.";
J. Endocrinol. 45:597-606(1969).
                     -i- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PIR; B61364; B61364.
PIR; S06375; S06375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-A. ACULEATUS;
MEDLINE-73223515; PubMed-4515919;
Acher R., Chauvet J., Chauvet M.-T.;
"Neurohypophysial hormones and evolution of tetrapods.";
Nature New Biol. 244:124-126(1973).
                                                                                                                                                                                                                                                                                                                                             Score 16; DB 1; Length 9;
Pred. No. 8.9e+04;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acher R., Chauvet J., Chauvet M.-T.; "Isolation of finback whale oxytocin and vasopressin."; Nature 201:191-192(1964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-H.AMPHIBIUS;
MEDLINE=71232719; PubMed=5406007;
Ferguson D.R., Pickering B.T.;
"Arginine and lysine vasopressins in the hippopotamus
                                                                                                                                                                                                                                        AMIDATION.
17EB176EB456D04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXYT_RABIT STANDARD; PRT; 9 AA. P32878; P01188; 21-JUL-1986 (Rel. 01, Created) 1-JUL-1986 (Rel. 01, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) OXYTOCIN (OCYTOCIN).
                                                                                                     INTERPRO; IPR000981; -.
FAM, PR000220; hormone4; 1.
PROSTTE; PS00264; NEUROHYPOPHYS_HORM; 1.
Hormone; Amidation.
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     HORMONE
                                                                                                                                                                                                                                                                                                                                          32.0%;
Similarity 66.7%;
2; Conservative
     -1- FUNCTION: ANTIDIURETIC
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9 9
9 AA; 1053 MW;
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Best Local Similarity
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4 QNC 6
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RESULT 8 ACPH_RABIT

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TISSUE=PITUITARY;
Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
"Characterization of neurohypophyseal hormones from a fresh water wony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes;
Elasmobranchii, Galeomorphii; Galeoidea, Carcharhiniformes;
Scyllorhinidae; Scyllorhinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyprinus carpio (Common carp).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinis.
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F2).
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                                                                                       INTERCHAIN (WITH C-6') (IN INTERCHAIN (WITH C-1') (IN
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                                                                                                                       AMIDATION.
56EB176EB451A057 CRC64;
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9 AA; 969 MW; 17FF476EB455B04B CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                        9 AA
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INTERPRO; IPR000981; -.
PFAM; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                         IN F1
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100.0%; Pre
                                                     Hormone; Neuropeptide; Amidation.
                                                                                                                                           9 AA; 976 MW;
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Best Local Similarity
2; Conserve
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Best Local Similarity
Matches 2; Conserv
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P42993;
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OXYA_SCYCA
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                                                            01-MXY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 32, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ACYCAMINO-ACID-RELEASING BUZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
(APH) (ACYLAMINOACYL-PEPTIDASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-SUBOESOPHAGEAL GANGLION, AND THORACIC GANGLION;
MEDLINE-88077077; PubMed=3689410;
Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
Delaage M., Schooley D.A.;
"Identification of an arginine vasopressin-like diuretic hormone from Locusta migratoria.";
Biochem. Biophys. Res. Commun. 149:180-186(1987).
-!- FUMCTION: DIORETIC HORMONE.
-!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                        Krishna R.G., Chin C.C.O., Wold F.,

"Veterninal sequence analysis of N alpha-acetylated proteins after
unblocking with N-acylaminoacyl-peptide hydrolase.",

Anal. Biochem. 199:45-50(1991).

-!-FUNCTION: THIS ENZYME CATALYZES THE HYDROLYZIS OF THE AMINO-
TERMINAL, PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERALE
AN N-ACETYLATED A AND A PEPTIDE WITH A FREE AMINO-TERMINUS.

IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.

-!-CATALYZIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
ACID + PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY.
                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Eukaryota; Metazoa; Arthropoda; Tradheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 1; Length 6; Pred. No. 8.9e+04; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AA; 775 MW; 6732D6C40B16F000 CRC64;
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01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).
                                   6 AA.
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PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
Hydrolase; Acetylation.
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                                   PRT;
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100.0%;
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                                 STANDARD;
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Best Local Similarity
Matches 3; Conserv
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                              ACPH_RABIT
P25154;
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P16339;
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MEDLINE-66123415; PubMed-5880565; Acher R., Crepy D.; Acher R., Chauvet M.-T., Crepy D.; Phylogeny of neurophyophyseal peptides: isolation of a new hormone, glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raja clavata (Thornback ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyvs;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
                                                                                                                                              Scyliorhinus canicula (Spotted dogfish) (Spotted catshark). Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Scyliorhindae; Scyliorhinus.
                                                                                                                                                                                                                                                     TISSUB-PITUITARY;
MEDLINE-95062247; PubMed-7972045;
MEDLINE-95062247; PubMed-7972045;
MEDLINE-95062247; PubMed-7972045;
MEDLINE-95062247; PubMed-7972045;

"Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytocin-like peptides isolated from the spotted dogfish (Scyllorhinus caniculus).";
Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
-I- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
-I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the ray (Raia clavata).";
slochim. Blophys. Acta 107:393-396(1965).
-!- FUNCTION: ANTIDIURETIC HORMONE.
-!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 15; DB 1; Length 9; 100.0%; Pred. No. 8.9e+04; Live 0; Mismatches 0; Indels
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9 AA; 1016 MW; 17EDD76EB44449DB CRC64;
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                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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                                       STANDARD;
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DISULFID 1
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                  PHASVATOCIN
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                                     OXYF_SCYCA
P42997;
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Acher R., Chauvet J., Chauvet M.-T.;
"Phytydeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";
Eur. J. Biochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acher R., Chauvet J., Chauvet M.-T., Fontaine M.; "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).".
C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchli; Squalea; Squaloidei; Squalidae; Squalus.
           TISSUE-PITUITARY;

MEDLINE=95062247; PubMed=7972045;

MEDLINE=95062247; PubMed=7972045;

"Special evolution of neuropypophysial hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytocin-like peptides solated from the spotted dogfish (Scyliothinus caniculus)."; Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).

-! FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
-! SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PRAM; PF00220; hormone4; 1.

PROSITE; PS002264; NEUROHYPOPHYS_HORM; 1.
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MW; 17F8376EB444404B CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
101-NOV-1995 (Rel. 32, Last annotation update)
ASPARTOCIN (ASPARCTOCIN)
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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01-JUL-1993 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
UNRNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 115) (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                    Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C., Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
"Human liver protein map. update 1993.";
Electrophoresis 14:1216-122(1993).
-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.5, ITS MW IS: 11 KDA.
SWISS-2DPAGE; P31931; HUMAN.
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SEQUENCE 9 AA: 1096 MW; 477B3B173AE729C7 CRC64;
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Query Match 30.0%; Score 15; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 8.9e+04; Matches 2; Conservative 0; Mismatches 0; Indels
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MEDLINE=94147969; PubMed=8313870;
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Solanales; Solanaceae; Nicotiana
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PARAT PROTEIN (FRAGMENT).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
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Tighe J.E., Calabi F.;
"Alternative, out-of-frame runt/MTG8 transcripts are encoded by the derivative (8) chromosome in the t(8:21) of acute myeloid leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.7e+05;
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01-NOV-1999 (TrEMBLrel. 12, Last annotation update) RUNT/82NT/MTG8 PROTEIN (FRAGMENT). RUNT/82NT/MTG8.
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PROMOTER 23 DNA FRAGMENT (FRAGMENT).
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EMBL, S74092; AAD14144.1; -.
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                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Recombinational junctions of variants of Moloney murine sarcoma virus: generation and divergence of a mammalian transforming gene."; J. Virol. 45:607-617(1983).

EMBL; K03105; AAA46490.1; -.
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SEQUENCE FROM N.A.

Niwa Y., Muranaka T., Baba A., Machida Y.;

"Organ specific and auxin-inducible expression of two tobacco parA-
related genes in transgenic plants.";

DNA Res. 0:0-0(1994).

EMBL; D42119; BAA07700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reconstruction: application to sequencing the amino-terminal coding region of the transforming gene of Gazdar murine sarcoma virus."; Nucleic Acids Res. 10:2549-2564(1982).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 3.7e+05;
0; Mismatches 1; Indels
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Last annotation update)
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Last sequence update)
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                                                                                                                                                                              905 MW; FE32D2C44455BB16 CRC64;
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                                                                                                                                                                                                                                                    30.0%;
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01-NOV-1996 (TrEMBLrel. 01,
01-MAY-1999 (TrEMBLrel. 10,
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MEX40.
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Matches 3; Conserv
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Crawford-Mikaza L.K., Nang R.N., Schnurr D.P.;
Crawford-Mikaza L.K., Nang R.N., Schnurr D.P.;
Wolecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenovirus type 7.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10519;
                         Lazarowitz S.G.;
"Molecular characterization of two bipartite geminiviruses causing squash leaf curl diseas: role of viral replication and movement functions in determinate host range.";
Virology 180:70-80(1991).
Virology 180:70-80(1991).
NON TER.
SEQUENCE 9 AA; 1118 MW; 2B30D5B457645417 CRC64;
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"Molecular characterization of two bipartite geminiviruses causing squash leaf curl disease: role of viral replication and movement functions in determining host range.";
Wirology 180:70-80(1991).
WHEL; MG3157; AAA47822.1;
NON TER
SEQUENCE 9 AA; 1118 MW; 2B30D5B457645417 CRC64;
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Pred. No. 3.7e+05;
0; Mismatches 1; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PVI CORE PROTEIN (FRAGMENT).
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10829;
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MEDLINE=91082450; PubMed=1984669;
  MEDLINE~91082450; PubMed-1984669;
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Best Local Similarity 75.0%;
Matches 3; Conservative
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1 MPRN 4
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Q9YVE3;
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                                                                         MEDLINE=95400293; PubMed=7670464; MEDLINE=95400293; PubMed=7670464; MEDLINE=95400293; PubMed=7670464; Med M.L., Collins J., Gong W., Roe B., Wang Z., Bailey L.C., Sellinger B., Michaud D., Driscoll D.A., Emanuel B.S.; "Cloning a balanced translocation associated with DiGeorge syndrome and identification of a disrupted candidate gene."; MAI. Genet. 10:269-278 (1955).

MAI. Genet. 10:269-278 (1955).

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SEQUENCE 9 AA; 1137 MW; 734911A69446837B CRC64;
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MEDLINE-95038750; PubMed-7951241;
ARDALINE-95038750; PubMed-7951241;
Arai E., Ikeuchi T., Nakamura Y.;
"Characterization of the translocation breakpoint on chromosome 22q12. 2 in a patient with neurofibromatosis type 2 (NF2).";
Hum. Mol. Genet. 3:937-939(1994).
EMBL: S75841; AAD14190.2; -.
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 3.7e+05;
0; Mismatches 1; Indels
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01-NOV-1996 (TrEWBLrel. 01, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NEUROFIBROMATOSIS TYPE 2 (FRAGMENT).
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
VCBI_TaxID=10829;
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067605;
01.NOV-1996 (TrEMBLEL). 01, C1
01.NOV-1996 (TrEMBLEL). 01, L2
01.NOV-1998 (TrEMBLEL). 08, L4
A COMPONENT DNA (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%;
75.0%;
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Best Local Similarity 42.9%;
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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                            NCBI_TaxID=9606;
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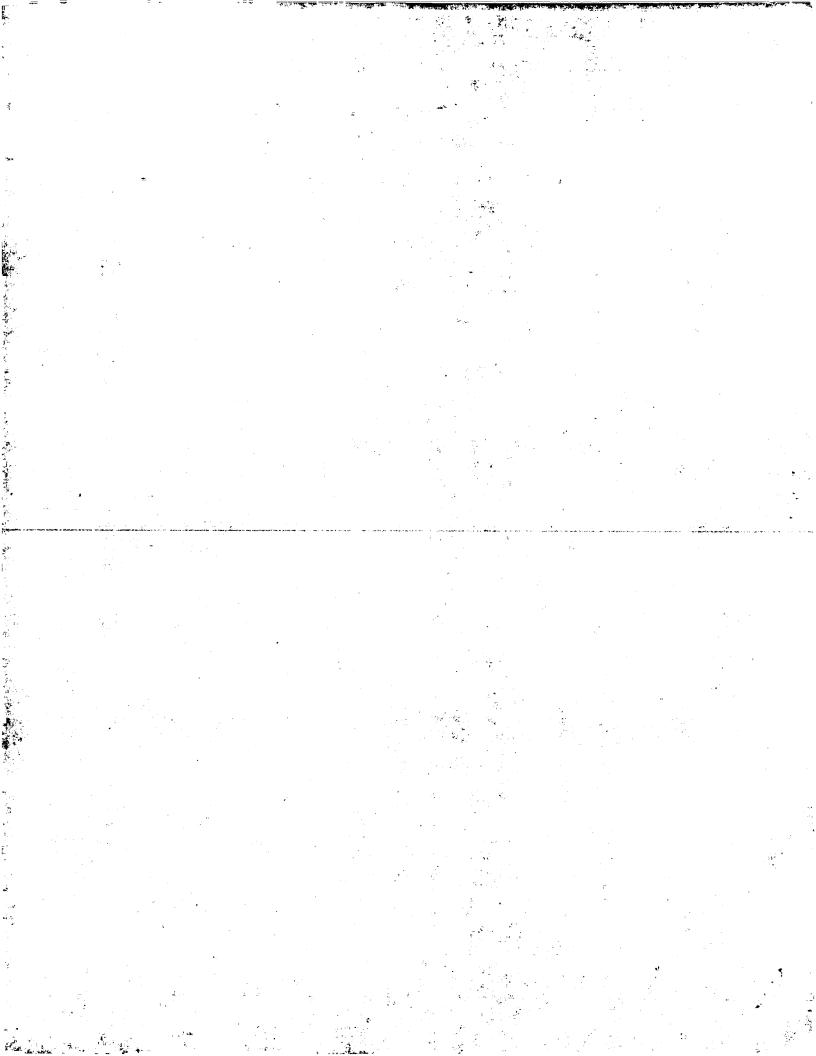
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MEDLINE-97426044; PubMed-9282748; Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D., Rosa P.; "The Borrelia burgdorferi circular plasmid cp26: conservation of plasmid structure and targeted inactivation of the ospc gene."; Mol. Microbiol. 25:361-374(1997).
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"he Bornelia burgdorferi circular plasmid cp26: conservation of plasmid structure and targeted inactivation of the ospC gene.";
Mol. Microbiol. 25:361-374(1997).
EMBL: U93693; ARC45521.1; -.
SEQUENCE 9 AA; 1005 MW; 4864C5B731A44333 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia garinii.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBL_TaxID=29519;
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
00-TER SURFACE PROTEIN C (FRAGMENT).
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                                                                 Score 14; DB 12;
Pred. No. 3.7e+05;
0; Mismatches 1;
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llarity 50.0%; Pred. No. 3.7e+05;
Conservative 2; Mismatches 0;
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Pred. No. 3.7e+05;
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50.0%;
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66.7%;
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Best Local Similarity
2; Conserve
                                                                 Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
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1 MKKN 4
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SEQUENCE
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STRAIN-KN T96-0620, S-1058, CL 68578;
Trayford-Miksza LK., Nang R.N., Schnurr D.P.;
Submirted (Max-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF065068; AAD03668.1;
EMBL, AF065068; AAD03668.1;
EMBL, AF065067; AAD03666.1;
SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;
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STRAIN=2-G 95-873, R1-67, 55142;
Crawford-mikaza L.K., Nang R.N., Schnurr D.D.;
Grawford-mikaza L.K., Nang R.N., Schnurr D.D.;
Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitteed (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF065064; AAD03659.1; --
EMBL, AF065064; AAD03659.1; --
EMBL, AF065063; AAD03659.1; --
EMBL, AF065063; AAD03650.1; --
EMBL, AF065063; AAD03659.1; --
EMBL, AF065064; AAD03659.1; --
EMBL, AF065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adenovirus type 7a.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=85755;
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=28280;
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Pred. No. 3.7e+05;
0; Mismatches 1; Indels
                                                                                                                                          Length 7;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TEMBLrel. 10, Last annotation update)
                                                           7B5EA414140322A0 CRC64;
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Pred. No. 3.7e+05;
0; Mismatches 1,
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EMBL; AF065065; AAD03662.1; -.
NON_TER 1 1
SEQUENCE 7 AA; 980 MW: 7855
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66.7%;
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66.7%;
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Best Local Similarity
Matches 2; Conserv
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Matches 2; Conserv
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STRAIN-PKO, IP21, AND J1;
STRAIN-PKO, IP21, AND J1;
Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
Rosa P.;
"he Borrelia burgdorferi circular plasmid cp26: conservation of
plasmid structure and targeted inactivation of the ospC gene.";
Mol. Microbiol. 25:361-374(1997).
EMBL; U93698; AAC45521.1;
EMBL; U93698; AAC45527.1;
ONON_TER
SEQUENCE 9 AA: 1005 MW; 4864C5B731A44333 CRC64;
        Gaps
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        0; Indels
                                                                                                                                                                                                                                                                                                                                                 OGR3TO PRELIMINARY; PRT; 9 AA.
OGR3TO: 09R3TO: 01-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
SOFT-
BOTTELIA afzelli.
BACTERIA: Spirochaetales; Spirochaetaceae; Borrelia.
2; Mismatches
2; Conservative
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1 MKKN 4
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1 MKKN 4
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09R3T0
AC 09R3T0
DT 01-MAY
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Search completed: January 17, 2001, 13:44:43 Job time: 197 sec



Sequence 31,

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/671,757
FILING DATE: 19910408
CLASSIFICATION: 530
CLASSIFICATION: A 61 K 37/02
PRIOR APPLICATION NUMBER: GB 8821785.6
ATTORNEY/AGENT INFORMATION:
NAME: FILING DATE: 16-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REGISTRATION NUMBER: 26,382
REGISTRATION NUMBER: 26,382
REGISTRATION NUMBER: 26,382
TELEFONEY (703) 683-1080
TELEFAN: (703) 683-1080
TELEFAN: (703) 683-1080
TELEEX: GROSSED ID NO: 18:
SEQUENCE CHARACTERISTICS:
US-08-485-886-195
US-08-477-1362-195
US-08-477-134-195
US-08-477-134-195
US-08-173-5108-66
US-08-173-5108-66
US-08-155-118-47
US-08-458-118-64
US-08-459-118-64
US-07-671-757-25
US-07-671-757-25
US-08-049-744-31
US-08-742-744-31
US-08-742-744-31
US-08-65-334-31
US-08-65-334-31
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US-08-65-34-31
US-08-65-34-31
US-08-65-34-31
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/note= "pyroglutamine"
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                                                                                                                                                                                                                                                                                                                                 PEPTIDE COMPOUNDS
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States of America
ZIP: 22314
                                                                                                                                                                                                                                                                                 Sequence 18, Application US/07671757
Patent No. 5484770
GENERAL INFORMATION:
APPLICANT: LAERUM, Ole D
TITLE OF INVENTION: PEFTIDE COMPOUN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NO
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HYPOTHETICAL: NO
FEATURE
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-07-671-757-18
  US-07-671-757-18
   Sequence 18, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appl
Sequence 25, Appl
Sequence 12, Appl
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5.187 Million cell updates/sec
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                                                                                 ; Search time 31.16 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS.COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                              174772 seqs, 17957048 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 January 17, 2001, 13:42:57
                                                            OM protein - protein search, using sw model
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                                                                                                                             US-08-765-837-8
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Match Length
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Score

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HAVING CORRESPONDENCE WITH HUMAN HEPATITIS
B SURFACE ANTIGEN
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ZIP: 14108
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: VICTOR 300 SX/25
COMPUTER: VICTOR 300 SX/25
COMPUTER: VICTOR 300 SX/25
COMPUTER: WORDSTAR PROFESSIONAL RELEASE 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,962
FILING DATE: 05-APR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/167,336
FILING DATE: 15-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, MICHAELL.
REGISTRATION NUMBER: 25,330
REFERENCE/DOCKET NUMBER: 25,330
REFERENCE/DOCKET NUMBER: 25,330
REFERENCE/DOCKET NUMBER: 25,330
TELEPHONE: (716) 433-1661
TELEPHONE: (716) 433-1665
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: DUNN & ASSOCIATES, P.C. P.O. BOX 96
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-167-336A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/03416962; Patent No. 5668253; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: THANAVALA, YASMIN
APPLICANT: THAKUR, ARVIND
APPLICANT: ROITT, IVAN
APPLICANT: PRIDE, MICHAEL
TITLE OF INVENTION: HAVING CORF
TITLE OF INVENTION: HAVING CORF
TITLE OF SEQUENCES: 12
                                 UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
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ADDRESSEE: DUNN & AS
STREET: P.O. BOX 96
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Matches 3; Conserv
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STATE: NEW YORK
         MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||
6 DRNC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ERNC 7
                                                                                                                                                                                                                                                                                                     JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-416-962-6
                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                              ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08167336A
Patent No. 551990
GENERAL INFORMATION:
APPLICANT: THARNVALA, YASMIN
APPLICANT: THAKUR, ARVIND
APPLICANT: PRIDE, MICHAEL
TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY
TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS
TITLE OF INVENTION: B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                  .;
0
      Score 23; DB 1; Length 5;
Pred. No. 1.3e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NEW YORK
COUNTEY: USA
ZIP: 14108
ZIP: 14108
ZIP: 14108
ZIP: 14108
COMPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: VICTOR 300 SX/25
OPERATING SYSTEM: MS-DOS VERSION 5.0
SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,336A
FILING DATE: 15-DEC-1993
CLASSIFICATION DATA:
FILING DATE: FILING DATE:
FILING DATE: TOWNMER: STATE STAT
                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DUNN & ASSOCIATES, P.C. STREET: P.O. BOX 96 CITY: NEWFANE
      46.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (716) 433-1661
TELEFAX: (716) 433-1665
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 60.0°
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
INDIVIDUAL ISOLATE:
DBVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL ITYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-6ENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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1 EQNCK 5
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US-08-167-336A-6
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CLONE:
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Live 1; Mismatches 0; Indels
 COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: VICTOR 300 SX/25
OPERATING SYSTEM: MS-DOS VERSION 5.0
SOCTWARE: WORDSTAR PROFESSIONAL RELEASE 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,011
FILING DATE: 19-JAN-1996
CLASSIFCATION 1 424
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/167,336
FILING DATE: 15-DEC.1993
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, MICHAEL L.
REGISTRATION NUMBER: 25,330
RECISTRATION STATEMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 433-1661
TELEFACOMMUNICATION NO. 6:
SEQUENCE: CARRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-589-011-6
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGNENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LIVE:
CELL LIVE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
LIBRARY:
LIBRARY:
CICONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
NAME/KEY:
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JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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US-08-589-011-6

Sequence 6. Application US/08589011
Patent No. 5744135
GENERAL INFORMATION:
APPLICANT: THARNVALA, YASMIN
APPLICANT: THARNVALA, ARVIND
APPLICANT: PRIDE, MICHAEL
TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY
TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS
TITLE OF INVENTION: B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUNN & ASSOCIATES, P.C.
STREET: P.O. BOX 96
CITY: NUMBER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14108
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Query Match

44.0%; Score 22; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-416-962-6
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                       LAUGUMENTAL
HAPLOTYPE:
TISSUE TYPE:
CELL LIVE:
CRELL LINE:
CREARELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                    INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
                                                                                           ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
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VOLUME:
ISSUE:
PAGES:
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Gaps

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Gaps
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US-09-074-912-11
Sequence 11, Application US/09074912
Septicant Capia, Amy I
APPLICANT CIGAN, AMY I
APPLICANT SEQUENCE COUT A
APPLICANT MENDER, ESCOTT A
APPLICANT SCHUBERT, KAREL
TITLE OF INVENTION: PROTEINS HAVING INSECTICIDAL ACTIVITIES
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. MURRAY .--
STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: W. MURRAY SPRUILL (ALSTON & BIRD, LLP)
STREET: 3605 GLENWOOD AVE.
CITY: RALBIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTER: USA
ZIP: 27622
COMPUTER READABLE. FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,912
                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 2; 1
Pred. No. 1.3e+05;
1; Mismatches 0
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                                                                                                                                                                                                                          FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-948-762-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SPRUILL, W. MURRAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEFAX: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     44.0%;
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                   OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 amino acids
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                   DATE:
DOCUMENT NUMBER:
                                                                             TITLE:
JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ERNC 7
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                                                                                                                                          ISSUE:
PAGES:
                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THANAVALA, YASMIN
APPLICANT: THANAVALA, YASMIN
APPLICANT: THANAVALA, YASMIN
APPLICANT: THANAVALA, TOUTT, IVAN
TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY
TITLE OF INVENTION: BSURFACE ANTIGEN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSED: DUNN & ASSOCIATES, P.C.
STREET: P.O. BOX 96
CITY: NEWFANE
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: VICTOR 300 SX/25
OPERATING SYSTEM: MS-DOS VERSION 5.0
SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREIGHTON NUMBER: 08/589,011
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 08/167,336
FILING DATE: 15-DEC-1993
ATTONNEY,FAGENT INFORMATION:
NAME: DUNN, MICHAEL L.
REGISTRATION NUMBER: 25,330
REFERENCE/DOCKET NUMBER: 25,330
                                                                               Sequence 6, Application US/08948762
Patent No. 5856087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (716) 433-1661
TELEFAX: (716) 433-1665
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: PEPTIDE HYPOTHETICAL: NO ANTI-SENSE: FRAGMENT TYPE: ORIGINAL SOURCE: ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: UNKNOWN TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 14108
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                     JS-08-948-762-6
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Patent No. 5529921
GENERAL INFORMATION:
APPLICANT: Peterson, Per A
APPLICANT: Jackson, Michael
APPLICANT: Lenglade-Demoyen, Pierre
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rammensee, Hans-Georg
APPLICANT: Rammensee, Hans-Georg
APPLICANT: Falk, Kirsten
APPLICANT: R tzschke, Olaf
APPLICANT: Stevanovic, Stefan
APPLICANT: Jung, G nther
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
                                                                                                                                                                      ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 5529921th Torrey Pines Road, TPC
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                                                                                                                             COUNTY TERDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLAD PC Compatible
COMPUTER: Eloppy disk
COMPUTER: BLAD PC Compatible
COMPUTER: DEAD PC COMPATION
CONFRONT APPLICATION DATA:
APPLICATION NUMBER: US 797
FILING DATE: 10-MAR-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/841,662
FILING DATE: 19-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, APTI
REGISTRATION NUMBER: SPF001P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEG 1D NO: 25:
SEQUENCE CHARACTER STICS:
LEFENDER: Q amino acids
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1.3e+05;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.0%; Score 21; DB nilarity 100.0%; Pred. No. 1.3 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-146-145-12; Sequence 12, Application US/08146145; Patent No. 5747269; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE: internal US-08-209-797-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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CITY: Washington
STATE: D.C.
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4 ENME 7
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Patent No. 5314813
GENERAL INFORMATION:
APPLICANT: Peterson, Per A
APPLICANT: Lenglade Demoyen, Pierre
APPLICANT: Lenglade Demoyen, Pierre
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
NUMBER OF SEQUENCE: 36
CORRESPONDENCE ADDRESS:
                                                              DB 3; Length 8;
1.3e+05;
                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: The Scripps Research Institute
STRET: 10666 No. 5314813th Torrey Pines Road, TPC
CITY: La Jolla
COUNTRY: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,662
FILING DATE: 19920219
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                            42.0%; Score 21; DB 100.0%; Pred. No. 1.3 rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Logan, April
REGISTRATION NUMBER: 33,950
REFRENCE/DOCKET NUMBER: SPF001P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEPRAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENTH: 9 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-209-797-25
; Sequence 25, Application US/08209797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                        Query Match
Best Local Similarity 100.v
Local 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FRAGMENT TYPE:
US-07-841-662-25
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                                                                                                                                                  1 ENME 4
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US-09-074-912-11
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APPLICANT: Edelson, Richard L.
APPLICANT: Edelson, Richard L.
APPLICANT: Edelson, Farancis P. Tancis P.
TITLE OF INVENTION: Cellular Vaccine and Methods of Use for TITLE OF INVENTION: the Treatment of Solid Tumor Malignancies NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield & Sacks, P.C.
SIREET: 600 Atlantic Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,691
FILING DATE: 19930730
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977672
FILING DATE: 18-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERNEC_DOCKET NUMBER: Y0060/7005
TELECOMMUNICATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  REGISTRATION NUMBER: P-35, 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/08100691
; Patent No. 5820872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.0%; Sc
Best Local Similarity 100.0%; P
Matches 4; Conservative 0;
                      REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             Query Match 42.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-054-860-1
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                                                                                         LENGTH: 9 amino a
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US-08-100-691-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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US-08-100-691-1
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CCMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,860
FLING DATE: 19930427
CLASSIFICATION 1514
PRIOR APPLICATION 1514
PRIOR APPLICATION NUMBER: SE 9201338-2
FILING DATE: 28-APR-1992
PROR APPLICATION NUMBER: SE 9201338-2
PRIOR APPLICATION NUMBER: SE 9202553-5
FILING DATE: 07-SEP-1992
                                    COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jondal, Mikael
TITLE OF INVENTION: New Active Compounds
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: White & Case STREET: 1155 Avenue of the Americas CITY: New York STATE: NY
                                                                                                                                                                         APPLICATION NUMBER: US/08/146,145
FILING DATE: 17-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203897-5
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: SE 9301141-9 FILING DATE: 06-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
TELEPOMMUNICATION INFORMATION:
TELEPHONE: (202)638-500
TELEPHONE: (202)638-4810
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08054860 Patent No. 5807559 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sterner, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-146-145-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA ZIP: 10036-2787 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
RY: U.S.A.
20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ENME 4
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Sequence 25, Application US/09103486
| Patent No. 6001365
| GENERAL INFORMATION
| APPLICANT: Deterson, Michael
| APPLICANT: Lenglade-Demoyen, Pierre
| TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
| NUMBER OF SEQUENCES: 6
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: The SCTIPPS Research Institute
| STREET: 10666 No. 6001365th Torrey Pines Road, TPC 8
| CITY: La Jolla
| STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,486
                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,035A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.0%; Score 21; DB 2; Lv 100.0%; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/517,373
FILING DATE: 21-AUG-1995
ATTONNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06765/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-6970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERA: 617/342 ...
TELERA: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHRACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNISS: not relevant
"nonLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,685
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                    225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 4; Conservative
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  ADDRESSEE: Fish &
                                                                                                        02110-2804
      USA
                                                                                        USA
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4 ENME 7
                                                               STATE: MA
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US-09-103-486-25
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                                                                                 Sequence 25, Application US/08669685
; Sequence 25, Application US/08669685
; Patent No. 5827737
; GENERAL INFORMATION:
    APPLICANT: Peterson, Per A
    APPLICANT: Jackson, Michael
    APPLICANT: Langlade-Demoyen, Pierre
    TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
    NUMBER OF SEQUENCES: 36
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: The Scripps Research Institute
    STREET: 10666 No. 5827737th Torrey Pines Road, TPC 8
    CITY: La Jolia
    STATE: California
    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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APPLICANT: Nair, et al., Smita K.
APPLICANT: Nair, et al., Smita K.
TITLE OF INVENTION: A METHOD TO INCREASE THE DENSITY OF
TITLE OF INVENTION: ANTIGEN ON ANTIGEN PRESENTING CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Logan, April
REGISTRATION NUMBER: 33,950
REFERENCE/COCKET NUMBER: SPF0001P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEPHONE: (619) 554-2937
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,797
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: US 07/841,662
FILING DATE: 19-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08700035A Patent No. 5831068
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9 amino acids
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4 ENME 7
                                                             RESULT 12
US-08-669-685-25
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Sequence 138, Application US/08481985B
Sequence 138, Application US/08481985B
Sequence 138, Application US/08481985B
Sequence 138, Application Gallide
APPLICANT: Mostez, Estelle
APPLICANT: Mostez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Mosterd Major Histocompatibility Complex
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION: Altered Major Histocompatibility Complex
STREET: 1300 I Street, N.W., Suite 700
CITY: Mashington
STATE: D.C.
ZIP: 20005-315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/481,985B
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/481,885B
FILING DATE: 15-NOV-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/481,885B
FILING DATE: 15-NOV-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/481,885B
FILING DATE: US/08/481,985B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 42.0%; Score 21; DB 3; Le Best Local Similarity 100.0%; Pred. No. 1.3e+05; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/POCKET NUMBER: 03495.0106-04000
TREECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                              FILING DATE: 19 FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SPF0001P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-6312
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                             US 07/841,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-09-103-486-25
                                                                                                                                                                                                                                                                                                                                                                                        ss: single
linear
FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENME 4
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4 ENME 7
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TEMERAX: 202-408-4400

JINFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
JOBECULE TYPE: peptide
US-08-481-985B-138
OUETY MATCH
42.0%; Score 21; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
MATCHES 4; CONSERVATIVE 0; Mismatches 0; Indels 0; Linps

QY 1 ENME 4

| | | | |
Db 4 ENME 7

Search completed: January 17, 2001, 13:42:58
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0

BLOSUM62

Scoring table:

Title: Perfect score:

Sequence:

protein

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Run on:

Minimum DB seq length: 0 Maximum DB seq length: 9

Database

Total number of

Searched:

. u

8; Page 13; 45pp; French.

Claim

factor VIII binding

Glycolipid sugar c Anaphylatoxin anta Prostate-specific Prostate-specific Human SULUI-derive

W02239 X55970

128432110

Score

Result Š

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Raf protein; effector loop domain; Ras; signal transduction; mediated signal transduction pathway; cell proliferation; binding; inhibition; Raf activation inhibiting activity; cell proliferation inhibition; ell proliferation inhibition; mmune cell receptor-mediated activation.
                                                                                                                                                                                                                                                                                                                                                                                                              Screening compounds which inhibit direct protein interaction useful to identify inhibitors of binding of Ras to Raf, Raf activation and cell proliferation
                                                                                                          Effector loop domain (amino acids 32-40) of Ras.
                                   W34647 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                Marshail MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 3; 50pp; English.
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50.0%;
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96US-0013274.
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                                                                                  01-APR-1998 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          11-MAR-1997;
                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                     12-MAR-1996;
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                                                           W34647;
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          Peptides R90945-64 are derived from the factor VIII protein, esp. from a modified Factor VIII in which residues Ala322-Ser750, Leu1655-Arg1689, Lys1694-Pro1782 and Asp2170-Tyr2332 are deleted. The modified Factor VIII and derived peptides can be used to prevent the activity of inhibitors of factor VIII binding to von Willebrand factor, esp. antibodies, thus preventing or treating immune disorders.
                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compounds with putative anti-oncogene or tumor suppressor activity are assayed by their ability to bind a Ras-binding fragment of Raf oncoprotein, such as the peptides given in R66644-49 and R6655-56, or to bind a Raf-binding fragment of Ras, such as the peptides given in R66650-52.
                                                                                                                                                                                                                                                                                                                                                               Oncoprotein; oncogene protein; Raf; Ras; zinc-finger domain; cancer; therapy; autoimmune disease; anti-proliferative; antitumor; anti-oncogene; tumor suppressor.
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                                                                                                                                 Length 9;
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                                                                                                                                 Score 52; DB 17;
Pred. No. 2.1e+05;
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating cancer and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 66; 94pp; English.
                                                                                                                                                                                                                                                                                                                                         Ras(32-40) oncoprotein fragment
                                                                                                                                                                                                                                                                  R66651 standard; Peptide; 9 AA.
                                                                                                                                 100.0%;
100.0%;
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ilarity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                               03-AUG-1995 (first entry)
                                                                                                                                                         9; Conservative
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                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 4; Conserv
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The present sequence represents amino acids 32-40 of Ras, which comprise the effector loop domain. The effector loop domain binds to amino acids 50-150 (w34649) of the Raf protein. This interaction participates in the transduction of an intracellular signal via the Ras RAf imediated signal transduction pathway which culminates in cell proliferation. A novel method for reducing cell proliferation in a mammal comprises administering to or contacting the cells with a compound which inhibits direct binding of the effector loop domain of Ras with an amino the present sequence. The methods are used to screen compounds for Raf activation inhibiting activity, cell proliferation inhibition and inhibition of direct binding of Ras to Raf. Blocking association of Ras with Raf interferes with receptor-mediated activation of immune cells. The method may also be useful in down-regulating the immune response in patients with autoimmune diseases such as systemic lupus erythematosus, type I diabetes, and rheumatoid arthritis.
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2.1e+05;
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Pred. No. 2.1e+
3; Mismatches
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ID W79899 standard; Peptide; 9 AA.
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W79899;

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This represents a Ras-binding peptide fragment of the Raf protein. The Ras-binding peptides especially those shown in W57456 to W57460 can be used in methods of inhibiting cell proliferation on an animal which comprises inhibiting direct interaction of Ras with Raf by administering the peptides. The Raf peptide can be used in methods of evaluating an anti-proliferative compound by contacting the compound with a Raf and determining its ability to bind to Ras. The peptides are useful for treating diseases characterised by disregulated signal transduction or aberrant cell proliferation, e.g. tumours and autoimmune diseases.
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                                                                                                                                                                                                                 Inhibition of Ras-Raf interaction in vivo - by administration of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29; DB 19;
Pred. No. 2.1e+05;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                  Disclosure; Column 2; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avruch J, Marshall MS, Zhang X;
                                                                                                                                                 Avruch J, Marshall MS, Zhang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W48229 standard; peptide; 9 AA.
                             94US-0259672.
93US-0077256.
95US-0460533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.8%;
50.0%;
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93US-0077256
95US-0460533
                                                                                                (GEHO ) GEN HOSPITAL CORP. (INDV ) UNIV INDIANA FOUND.
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Best Local Similarity
Matches 4; Conserv
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2 dptiedsy 9
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11-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1994;
02-JUN-1995;
                                 10-JUN-1994;
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02-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raf; Ras; Ras-binding fragment; inhibition; tumour; autoimmune disease; disregulated signal transduction; cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding NOEY2 tumour suppressor from ovarian epithelium - useful for, e.g. treatment, diagnosis and prognosis of cancer, particularly cancer of ovary and breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the effector domain of Ras and Rap family members. A putative effector domain of NOEY2 (see W79898) differs in 3 residues from this sequence. NOEY2 is a novel human tumour suppressor protein that is absent or down-regulated in breast and ovarian cancers. NOEY2 polynucleotides (see V60577-78) and polypeptides of the invention are used in the treatment, diagnosis and prognosis of cancer, particularly of the ovary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ras-binding fragment of Raf protein Raf(32-40) (residues 32-40).
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                                                                                            NOEY2; tumour suppressor; human; breast cancer; ovary cancer; diagnosis; therapy; transgenic animal; vaccine; Ras; Rap;
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2.1e+05;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 102; 182pp; English.
                                                              Ras and Rap family effector domain.
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97US-0041580.
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Best Local Similarity
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21-MAR-1997;
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WPI; 1998-537487/46.
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             Sequence
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                                 The present sequence represents a Raf-binding peptide fragment of Ras, from the present invention. The present invention describes: (1) a method of evaluating an anti-proliferative compound comprising contacting the compound with an amino-terminal, non-catalytic Ras-binding fragment of Raf and determining the ability of the compound to bind to the fragment, where the binding ability of the compound is an indication that the compound inhibits cell proliferation; and (2) a method of evaluating an anti-proliferative compound comprising contacting the compound with a Raf-binding fragment of Ras comprising an intact effector loop and determining the ability of the compound to bind to the fragment, where the binding ability of the compound is an indication that the compound inhibits cell proliferation. Antiproliferative compounds identified as above can be used to treat tumours and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A peptide of 5-25 amino acid residues (pref. one of the pentapeptides R37031-3 or an atriopeptin e.g. atriopeptin A or D, see R37337-8) having an activated carboxyl group capable of forming a betaglycosylamine linked glycoconjugate is reacted with an unprotected beta-glycosylamine deriv. of an oligosaccharide. The deriv. is prepared by reacting an unprotected oligosaccharide and enving up to 9 saccharide units with saturated ammonium bicarbonate at pH 8.0-8.5. The N-linked glycoconjugate is produced under conditions to directly maintain the beta-anomeric configuration.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-linked peptide glyco-conjugate(s) prepn. - by reacting oligosaccharide(s) with ammonium bi:carbonate to maintain beta-anomeric configuration, and avoid sepn. of anomers
                                                                                                                                                                                                                                                                Score 29; DB 19; Length 9;
Pred. No. 2.1e+05;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-anomer; beta-glycosylamine linked glycoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pentapeptide component #1 of N-linked glycoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong SYC,
            Claim 10; Column 35-36; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 32; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                 R37031 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                h 55.8%;
Similarity 50.0%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92EP-0870165
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92US-0926786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                           9 AA;
                                                                                                                                                                                                                                                                                                                       1 DPTFKENY 8
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2 dptiedsy 9
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glyco-lipid sugar chain replica peptide - reacts specifically with antibody against glyco-lipid sugar chain and controls glycosidase activity, useful for improving treatment of liver diseases
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DB 14; L
2.1e+05;
hes 0;
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Pred. No. 2.1e+05;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                               Glycolipid sugar chain replica peptide #LCO7.
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46.2%; Score 24; DB 100.0%; Pred. No. 2.1
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ID R30572 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                W71343 standard; peptide; 9 AA.
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57.1%;
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                                                 Conservative
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Anaphylatoxin; receptor; ligand; antiinflammatory; hexapeptide; heptapeptide; immunodeficiency; allergy; autoimmune; ARDS; cancer; infection; endetoxin, asthma; gout; psoriasis; cirrhosis; inflammatory; bowel; disease; hepatitis; burns; myocardial; infarction; transplant rejection; ischaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate-specific membrane antigen; PSM; prostate cancer; transmembrane glycoprotein; imaging; targeting; tumour detection; antibody detection; sequencing.
                                                                                                                                                                                                                                                                                                                             New hexa- and hepta:peptide(s) are anaphylatoxin antagonists and agonists - for treating inflammatory and immunodeficiency diseases, cancers and severe infections
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                                                                                                                                      'note= "(2R)-2-amino-3-cyclohexyl-propanoyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 13; Length 6; Pred. No. 2.1e+05;
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                                                                                                                                                                                                                                                                                     Wagner R,
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 154; 160pp; English.
                                                                                                     'note= "N-Me-Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R55100 standard; Peptide; 7 AA.
                                                                                                                                                         /note= "D-Arg"
                                                                                                                           'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.28;
66.78;
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                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                     Or YS,
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                                                                                                                                                                                                                                                                                     Kawai M, Luly JR,
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Matches 4; Conserv
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                                                                                            Modified-site
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                                                              Synthetic
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The inventors attempted to sequence the PSM Ag by modified Edman degradation. Peptides (R55098-107) that gave clear dominant peaks on HPLC from the digested PSM Ag sample were used. Some of the residues were unidentified, and others were present at very low residues were unidentified with lower confidence. Some of these peptides were used to design primers to carry out PCR to identify cDNA clones cancoding the PSM Ag. R55100 was used to design primers 065521 and 06552. A clone, IN-20 was identified as a partial PSM sequence. CO5522. A clone, IN-20 was identified as a partial PSM sequence. CO5520. The PSM coding sequence is useful for suppressing or modulating the metastatic ability of prostate tumour cells to grow, or for eliminating them. The proceed is useful to identify or purify iligands of the Ag. It is also an attractive target for Ab-directed imaging and targeting of prostatic tumour deposits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate-specific membrane antigen and DNA encoding it - 1s useful for detecting haematogenous micro-metastatic tumour cells and for identifying ligands which bind to PSM Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                 (SLOK ) SLOAN KETTERING INST CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example ; Page 44; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                Israeli
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Best Local Similarity
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Homo sapiens
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3 dpmfk
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This sequence represents a peptide fragment from a novel STE20-related protein kinases. The invention relates to nucleic acid molecules encoding a kinase polypeptide selected from STLK2, STLK4, STLK5, STLK6, CSTLK7, 2C1, 2C2, 2C3, 2C4, KHS2, SULU1, SULU3, GEK2, PAR4 and PAR5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides such as immune-related disorders and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. crohn's disease), asthma, osteoarthritis, psoriasis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmuity, and organ transplantation, chronic inflammatory pelvic disease, multiple sclerosis, organ chronic inflammatory pelvic disease, multiple sclerosis, organ chronic inflammatory pelvic disease, multiple sclerosis, organ chronic lateral sclerosis, Parkinson's disease and Leigh syndrome), candioumyopathies, ischemic disorders, inflammatory disorders, cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may calso be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.
                                 Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunodeficiencies; immunosuppression; T-cell subset; immunotherapy; inflammation; wounds; lymphocyte; vaccine.
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Pred. No. 2.1e+05;
1; Mismatches 0; Indels
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                                                                                       Disclosure; Page 379; 387pp; English.
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80.08;
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 WPI; 1999-611301/52.
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Best Local Similarity
Matches 4; Conserv
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5 kedyr 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic; antibsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive; neuroprotective; cardiant; cerebroprotective; oytostatic; antidiabetic; vulnery; STE20; protein kinase; STEX3; STLK3; STLK4; STLK5, STLK6, STLK7, 2C1, 2C2, 2C3, 2C4, KHS2, SULU1, SULU3, GEK2, PAK4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oxidative stress related neurodegenerative disorder; Parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis; mesangial disorder; growth regulation; wound healing; T cell activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                 specific membrane (PSM) antigen (see also W02234) and used to closing primers (T36795-808) utilised in the isolation of a cDNA clone (T36785) coding for PSM; primers A and B (T3795-96) are based on amino acids 1-5 of peptide 2T26 3 (W02239). The isolated cDNA and PSM protein are useful in developing methods for the diagnosis and treatment of prostate cancer and metastasis.
                                                                                                                                                                                                                                                 (W02237-45) were obtd. from the human prostate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                               useful to develop prods. for detecting haematogenous
                                                                                                                                           DNA encoding alternatively spliced prostate-specific membrane
                                                                                                                                                                              micrometastic tumour cells, or prostate cancer progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 17; LA
Pred. No. 2.1e+05;
0; Mismatches 1;
                                   (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                               Example 1; Page 49; 284pp; English.
                                                                      Israeli RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whyte D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y55970 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human SULU1-derived peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                44.2%;
80.0%;
95US-0466381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US08150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0081784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martinez R,
                                                                      Heston WDW,
                                                                                                     WPI; 1996-402365/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressant.
                                                                                                                                                                                                                                                 Tryptic peptides
                                                                                                                                                                                                                                                                                                                                                                                          7 AA;
02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DPTFK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9953036-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 | 1
3 dpmfk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plowman G,
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                      Fair WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
                                                                                                                                                               antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X55970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ношо
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Gaps

us-08-765-837 -9.closed.rag

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Gaps

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The sequence is a specific example of a group of new immunogenic peptides having an HLA-A3.2 HLA-A1, HLA-A11 or HLA-A24.1 binding motific. For example, the peptides having an HLA-A3.2 binding motific each have 9-10 residues and contain, from the N-terminus to the C-terminus, (a) a first conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and (b) a second conserved residue of K, R, Y, H or F, where the first and second conserved residues are separated by 6-7 residues. The peptides are capable of binding selected MHC molecules and inducing an immune response. They can be used to treat and/or prevent viral infection and cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also be used to produce antibodies for use as diagnostic or therapeutic agents. The peptides can also be used as diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC; major histocompatability complex; viral infection; anticancer; prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide which specifically binds selected MHC allele - used to induce an immune response for treatment or prevention of viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 15; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 0; Indels
Score 22; DB 13; Length 8;
Pred. No. 2.1e+05;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cERB2 oncogene-derived HLA-binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection or cancer, or for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 103; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                             Y37952 standard; Peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.3%;
42.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Local 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-065403/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CYTE-) CYTEL CORP.
Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                        ||:|:::
1 tfeesfq 7
                                                                                                                              3 TFKENYR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9403205-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::||
5 fedny
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                                                                                                                                                                                                                                                                                                                                                                                                                               Y37952;
                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                               X37952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                The immunomodulatory peptide is a specific example of a peptide cpd. (or an acid or base salt) constructed by combination and/or overlapping of the amino acid sequences AlBINBA2A, ABB3XA4B4, BB5A5XA6B6, BAAXXB8AB, AB99, AlOAll, BIOAL2, and BIIBL2 (x= Ala, Gly, IIe, Leu, Phe or Val, Al-Al2 each= Arg, Asn, Gln, Lys, Phe or Val; B-B12 each= Asp, Glu, Tyr, Phe or Val. The synthetic peptide may be used for immunomodulation of various immunodeficiencies and immunosuppressed conditions, T-cell subset and lymphocyte deviations, enhancement of a vaccines efficacy, as well as for immunotherapy, including infections, local or systemic complications of non-infectious diseases, postoperative inflammations, wounds and burns. See also R24583-R24701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in R27983-8000 and R28044 are fragments from insulin receptor substrate-1 (IRS-1). These fragments were used to determine the sequence of IRS-1 and to distinguish it from proteins which are co-puried with it. Antibodies were raised against the IRS-1 proteins and were used to remove them from the reaction media. These peptides were formed by proteolytic cleavage of proteins isolated by 1D-SDS PAGE to be approx. 185 kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insulin receptor substrate-1; IRS-1; antibody; proteolytic cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purified nucleic acid encoding Insulin Receptor Substrate - used to prepare IRS-1, for diagnosis and treatment of insulin related diseases and abnormal cellular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 13; Length 6;
Pred. No. 2.1e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 26; 128pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rothenberg PL, White MF;
Claim 10; Page 36; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JOSL-) JOSLIN DIABETES CENT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R27999 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tryptic peptide fragment #17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910S-0643982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US00437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-365881/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 FKENYR 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1D-SDS PAGE
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Gaps

0;

Length 9;

Search completed: January 17, 2001, 13:42:25 Job time: 139 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 17, 2001, 13:43:38; Search time 36.59 Seconds (without alignments) 16.701 Million cell updates/sec

US-08-765-837-9 52 1 DPTFKENYR 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues Searched:

787 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11000		*				
	Score	Match	Length	DB	ID	Description
:	22	42.3	8	2	S21273	cellulase (EC 3.2.
	19		80	~	JS0317	IIV (
	19	36.5	σ	7	PT0324	Iq heavy chain CRD
	18	34.6	4	ď	S53508	starvation-induced
	18	34.6	80	~	S71919	alcohol dehydrogen
	17	32.7	80	7	966808	hypertrehalosemic
	17	32.7	80	ď	B49823	adipokinetic hormo
	17	32.7	ω	~	B44960	neuropeptide Led-C
	17	32.7	æ	7	A61597	cytochrome P450 AL
	16	30.8	8	7	S70727	ipgF protein - Shi
	16		6	7	A42266	peptidylglycine mo
	15	28.8	9	~	S11556	hydrogensulfite re
	15		8	7	S43971	tumor-associated a
	15		89	7	S43972	tumor-associated a
	15		σ	7	A61230	calsequestrin, car
	15		6	7	PT0270	Ig heavy chain CRD
	15		6	7	PT0285	Ig heavy chain CRD
	14	26.9	89	7	PT0030	inulinase (EC 3.2.
	14	26.9	6	7	A60108	exotoxin A - Strep
	13		4	7	151049	metallothionein-A
	13		5	7	B60274	major protein anti
	13		Ω.	7	PT0281	Ig heavy chain CRD
	13		φ	7	A19780	transferrin - bovi
	13		9	7	PT0709	T-cell receptor be
	13	25.0		7	S71867	glutathione transf
	13	25.0	7	~	A38081	amine oxidase (cop
	13	25.0		4	I56695	hypothetical L2 pr
	13	25.0	80	~	808995	hypertrehalosemic
	13	25.0	80	~	A49823	adipokinetic hormo

neuropeptide led-C adipokinetic hormo hypertrehalosemic hypertrehalosemic adipokinetic hormo cat-transportide - flo cat-transporting dihydroliposmide s adipokinetic hormo cat gene leader pe chloramphenicol O- quinoline zoxidor hutU protein Kie	
A44960 S15422 B43976 B43976 S11545 S11545 A58641 A65493 A65493 A65493 B45796 B24362 S30494 S30494 C36607	
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ALIGNMENTS

ALIGNMENTS		is of 1,4-beta-D-gluc gradation hydrolase; polysacc 42.3%; Score 22;	Hest Local Similarity 80.0%; Pred. No. 20+05; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 2 PTFKE 6	RESULT 2 JS0317 leucokinin VII - Madeira cockroach C;Species: Leucophaea maderae (Madeira cockroach) C;Deteies: D-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000	Riboland, G.M.; Cook, B.J.; Nachman, R.J. Comp. Blochem. Physiol. C 88, 31-34, 1987 A.Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the A; Reference number: JS0317 A.R.Cession: JS0317 A.R.Cession: JS0317 A.R.Cession: JS0317	A Modified Site: process a family of cephalomyotropic peptides, stimulate contractile C; Comment: Leucokinins, a family of cephalomyotropic peptide C; Keywords: amidated carboxyl end; cephalomyotropic peptide F; 8/Modified site: amidated carboxyl end (GLy) #status experimental.	Query Match 36.5%; Score 19; DB 2; Length 8; Best Local Similarity 75.0%; Pred. No. 2e+05; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gups 0;
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1 DPTF

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2

0

Gaps

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Length 8;

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hypertrehalosemic hormone II - oriental cockroach
NyAlternate names: Pea-CAH-II
NyAlternate names: Pea-CAH-II
C;Decies: Blatta orientalis (oriental cockroach)
C;Decession: 508996
C;Accession: 508996
R;Gade, G;Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corentalis and of the stick insect Extacosoma tiaratum assigned by tandem fast atom bomb
A;Reference number: 508995; MUID:90253659
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A;Residues: 'E', 2-8 <WIT>
C;Superfamily: adipokinetic hormone
C;Superfamily: adipokinetic hormone
E;U,Modified site: pyrrolidone carboxylic acid (Gln) #status experimuntal
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimuntal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adipokinetic hormone II - American cockroach
N;Alternate names: neuropeptide M-II; periplanetin CC-1
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: B49823; A05170
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and A;Reference number: A49823; MUID:84298179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-8 <SCA>
R; Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr.,
B; Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Ook, J.C.; Hemling, M.E.; Rinehart Jr.,
B; Witten, Diophys. Res. Commun. 124, 350-358, 1984
A; Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment
A; Reference number: A90118; MUID:85046530
A; Accession: A05170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Molecule type: protein
A. Residues: 1-8 GAES.
A. Residues: 1-8 GAES.
A. Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore,
C. Superfamily: adipokinetic hormone
C. Superfamily: adipokinetic hormone, neuropeptide; pyroglutamic acid
E:1/Revords: amidated carboxyl and; hormone, neuropeptide; pyroglutamic acid
F:1/Rodified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental
                    ore 18; DB 2; Lered. No. 2e+05;
Mismatches 0;
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Pred. No. 2e+05;
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Pred. No. 2e+05;
l; Mismatches
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                       Score 18;
34.6%; Scor.
100.0%; Pre
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50.0%;
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Best Local Similarity 50.0%;
Matches 3; Conservative
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Matches 3; Conserv
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2 DPT 4
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alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)
alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)
alcohol dehydrogenase (EC 1.1.1.1) - grass carp)
C:Specias: Ctenopharygodon idella (grass carp)
C:Accession: 571919
C:Accession: 571919
C:Accession: 571919
C:Accession: 571919
A:Trui, H.T.; Mock, W.T.; Eau, K.K.; Fong, W.P.
Biochim. Biophys. Acta 1296, 41-46, 1996
A:Trile: Proteolytic activation of grass carp (Ctenopharygodon idellus) liver alcohol de A:Reference number: 571919
A:Reference number: 571919
A:Reference number: 571919
A:Residues: 1-8 - TSUS
A:Molecule type: protein
A:Residues: 1-8 - TSUS
A:Residues: 1-8 - TSUS
A:Residues: 1-8 - TSUS
A:Note: the source is designated Ctenopharyngodon idellus
C;Reywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Lycopersicon esculentum (Comato)
C;Species: Lycopersicon esculentum (Comato)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C;Accession: S53508
R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
Plant Mol. Biol. 27, 477-485, 1995
A;Title: CDNA structure and regulatory properties of a family of starvation-induced ribc
A;Reference number: S53506; MUID:95201242
A;Accession: S53508
                                                                                                                                                                                                                                       C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: P70324
R;Yamada, M; Wasserman, R; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J; Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: P70222; MUID:91108337
A;Accession: P70324
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
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                                                                                                                                                                                                                     Species: Homo sapiens (man)
Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
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3. 2e+05;
0; Indels
                                                                                                                                                                                    Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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Pred. No. 2e+05;
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100.0%; Pre
0; }
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42.9%;
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Thes 3; Conserva
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A; Molecule type: protein
A; Residues: 1-4 <KOE>
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Best Local Similarity
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|DPAF 4
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hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fraquen N;Alternate names: bisulfite reductase; desulfofuscidin C;Specias: Desulfovibrio thermophilus (c)Specias: Desulfovibrio thermophilus (c)Specias: Desulfovibrio thermophilus (c)Specias: Desulfovibrio thermophilus (c)Accession: S11556 (c)Accession: S11556 (c)Accession: S11556 (c)Accession: S11556 (c)Accession: S11556 (c)Accession: S1100, A:R: Czechowski, M:; Kang, L.; DerVartanian, D.V.; Moura, J.J.G. Biochim: Biophys. Acta 1040, 112-118, 1990 (c)Accession: S11024; MUID:90335276 (d)Sulfite reductase (dusulfofuscidin) for Accession: S11024; MUID:90335276
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C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C;Accession: S43971
                                                                                                               Gaps
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A;Note: sequence extracted from NCBI backbone (NCBIN:82733, NCBIP:82750)
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40.0%; Pred. No. 2e+05;
iive 2; Mismatches
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ed. No. 2e+05;
Mismatches
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Pred. No.
                                                                    Score 16;
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40.0%;
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A; Residues: 1-6 <FAU>
C; Keywords: oxidoreductase
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Best Local Similarity
Matches 2; Conserv
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A; Residues: 1-9 <EIP>
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5 FKDTF 9
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2 KQNNR 6
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      A;Gene: ipgF
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C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C; Accession: A61597
R; Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
B; Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
B; Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
A; Title: Purification and aminopyrine monooxygenase activity of liver microsomal cytochr
A; Reference number: A61597; MUID:91292910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Allaoui, A.; Sansonetti, P.J.; Menard, R.; Barzu, S.; Mounier, J.; Phalipon, A.; Parsol Mol. Microbiol. 17, 461-470, 1995
A;Title: MxiG, a membrane protein required for secretion of Shigella spp. Ipa invasins:
A;Reference number: S70727; MUID:96100445
A;Accession: S70727
                                                                                                                                                               C;Accession: B44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and A;Reference number: A44960; MUID:90160053
                                                                                                                                                                                                                                                                                                                                                                               pyroglutamic
                                                                                                                                                                                                                                                                                                      A.Molecule type: protein
A.Residues: 1-8 «GAE»
S.Superfamily: adipokinetic hormone
C.Superfamily: adipokinetic hormone
C.Keywords: blocked carboxyl end: corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (GIn) #status experimental
F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
C;Genetics:
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                                                                                                           neuropeptide Led-CC-II - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
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C.Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
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Pred. No. 2e+05;
1; Mismatches
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2e+05;
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Pred. No. 2e+0:
1; Mismatches
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A;Molecule type: protein
A;Residues: 1-8 <SHI>
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calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (gragment)
N;Alternate names: 58k dihydropyridine-binding protein; aspartactin; calmitine; laminin-
C;Species: Rana pipiens (northern leopard frog)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A61230
C;Accession: A61230
R;McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991
A;Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular calmium.
A;Reference number: A61230; MUID:91316784
A;Accession: A61230
A;Molecule type: protein
A;Residues: 1-9 cACL>
C;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protein
C;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to c;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi
C;Superfamily: calsequestrin
C;Superfamily: calsequestrin
C;Keywords: calcium binding: cardiac muscle; glycoprotein; heart; phosphoprotein; skelet
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C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C;Accession: $43972
R;Mandelboim, O: Berke, G:; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine A;Accession: $43972
A;Status: preliminary
A;Status: protein
A;Residues: protein
A;Residues: 1-8 <AMAN>
C;Superfamily: unassigned animal peptides
R;Mandelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L. Nature 369, 67-71, 1994
Nature 369, 67-71, 1994
N;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine A;Reference number: 543971; MUID:94217811
A;Reference number: A33971
A;Reference number: Protein A;Residues: protein A;Residues: 1-8 cMAN-
C;Superfamily: unassigned animal peptides
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Peptides 13:209-214 (1992).
-!- FUNCTION: MYOACTIVE.
-!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS. . : :ATED
achut Ina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-93027659; Pubmed-1408999;
Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
Garrison R.D., Williams J.F., Friedman A.R.;
"Two FMRPamide-like peptides from the free-living nematode
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Holman G.M., Cook B.J., Nachman R.J.;
Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUDALLY TO THE BASE OF THE PHARYNX.
SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
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Bukaryota, Metazoa; Arthropoda; Tracheata: Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
  P35921
P14595
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
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C6D40729C4576AB5 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE PF1 (SDPNFLRR-AMIDE).
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Pred. No. 8.9e+04;
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Ol-WAY-1991 (Rel. 18, Last sequence update)
Ol-WAY-1991 (Rel. 18, Last annotation update)
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UPAA_HUMAN
MOSF_CLYJA
NEUX_HUMAN
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Copyright (c) 1993 - 2000 Compugen Ltd.
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HTF2_PERAM
LCK2_LEUMA
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ALL4_CARMA
FAR1_HELTI
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AKH_MELML
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ACI_THUAL
FAR7_ASCSU
LCK4_LEUMA
RS10_SALIY
COXE_THUOB
OXYT_EISPO
RS10_SERMA
TKC1_CALVO
UPA3_HUMAN
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HTF1_PERAM
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2_PANRE
                                                                                                                                    January 17, 2001, 13:47:10
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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HUTU
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length: 9
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Database

Perfect score:

Title:

Sequence:

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Run on:

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"Two FMRFamide-like peptides from the free-living nematode
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Best Local Similarity
Matches 3; Conserv
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3 DPNF 6
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P04549;
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P43170;
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SEQUENCE
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SEQUENCE
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SEQUENCE.
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HTF2_PERAM
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Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
Garrison R.D., Williams J.F., Friedman A.R.;
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comp. Blochem. Physiol. 88C:31-34 (1987).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: JO THE OTHER LEUCOKININS.
PIR; JS0317; JS0317.
                   Comp. Biochem. Physiol. 84C:205-211(1986).
-!- FUNCTION: THIS CEPHALDOWYORROLD: PETILDE STIMULATES CONTRACTILE
-!- COCKROACH PROTODEUM (HINGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holman G.M., Cook B.J., Nachman R.J.; Isolation, primary structure and synthesis of leucokinins VII and "Isolation, primary structure and synthesis of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.";
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0
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                                                                                                                                                                                                         Score 19; DB 1; Length 8; Pred. No. 8.9e+04; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 1; Length 8; Pred. No. 8.9e+04; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAR2_PANRE STANDARD; PRT; 9 AA. P41873; PAI. STANDARD; PAI. STANDARD; PRT; 9 AA. P41873; PAI. STANDARD; PAI. STANDARD; PAI. STANDARD; PAIR AMIDE LIKE NEUROPEPTIDE PF2 (SADPNFLEF-AMIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION.
DC6365A5B9CDC76A CRC64;
                                                                                                                          AMIDATION.
DC6365B449CDC76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update),
01-FEB-1991 (Rel. 17, Last annotation update)
LEUCOKININ VII (L-VII).
                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blaberoidea; Blaberidae; Leucophaea
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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0
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75.0%;
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ilarity 75.0%;
Conservative
                                                                                                                                              8 AA; 893 MW;
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                                                                                                      Neuropeptide; Amidation.
MOD_RES 8 8
SEQUENCE 8 AA; 893 MW;
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MOD_RES 8 8
SEQUENCE 8 AA; 866 MW;
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Cephalomyotropins.";
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LCK7_LEUMA
P19989;
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TO LCK7_LEUMA
AC P1-FEB
DT 01-FEB
DT 01-FEB
DE LEUCOP
OC PLEUCOP
OC PLEUCOP
OC Blaber
RN | 101|
RP | 115SUE
RR | 11
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  RT CCC RT SO SE TT SO
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-!- FUNCTION: MYOACTIVE.
-!- TRASUE SPECTRICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LACATED CAUDALLY TO THE BASE OF THE PHARYNX.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HYPERTREHALOSABMIC FACTOR II (WINDROPEPTIDE M-II) (PERIPLANETIN CC-2)
(PEA-CAH-II) (LED-CC-II) (HYPERTREHALOSAEMIC NEUROPEPTIDE II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cowden C., Stretton A.O.W.;
"Eight novel FWRFamide-like neuropeptides isolated from the nematode
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota, Metazoa, Nematoda, Chromadorea, Ascaridida, Ascaridoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascaris suum.";
Peptides 16:491-500(1995).
-!- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                 Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Periplaneta americana (American cockroach),
Leptinotarsa decemlineata (Colorado potato beetle), and
Blatta orientalis (Oriental cockroach).
                                                                                                                                                                                       AMIDATION.
DA0B0729C4576AAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
340B0059D1B76338 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 1; L4
Pred. No. 8.9e+04;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                 Score 19; DB 1; Pred. No. 8.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA.
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95380362; PubMed=7651904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMRFAMIDE-LIKE NEUROPEPTIDE AF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
01-FEB-1996 (Rel. 33, Last ann
                                                                                                                                                                                                                                                                                   36.5%;
75.0%;
                                                                                                                                                                                           9 9
9 AA; 1066 MW;
Panagrellus redivivus.";
Peptides 13:209-214(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA; 1052 MW;
                                                                                                                                                                                                                                                                            Query Match 36.5
Best Local Similarity 75.0
Matches 3; Conservative
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Neuropeptide; Amidation.
                                                                                                                                                              Neuropeptide; Amidation.
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neuropeptides

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Gaps

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1; Indels

9 AA.

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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
17PYPSIN MODULATING OOSTATIC FACTOR (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomouplus;
06stroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 106) (FRAGMENT).
HOMO sapiens (Human).
ELNATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6, ITS MM IS: 15 KDA.
                                                                                                                        Cephalomyotropins.";
Comp. Biochem. Physiol. 84C:205-211(1986).
- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILLE
- ACTIVITY OF COCKROACH PROTODEUM (HINGUT).
- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LIVER;
MEDLINE-94147369; PubMed-8313870;
Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
"Human liver protein map: update 1993.";
Electrophoresis 14:1216-1222(1993)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.9%; Score 14; DB 1; Length 9; 50.0%; Pred. No. 8.9e+04; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                32.7%; Score 17; DB 1; Length 8;
larity 75.0%; Pred. No. 8.9e+04;
Conservative 0; Mismatches 1; Indels
                                      TISSUE=HEAD;

Johnan G.M., Cook B.J., Nachman R.J.;

Flolanio, primary structure and synthesis of two if from Lucophaea maderae: members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D02DFB41B6D33322 CRC64;
                                                                                                                                                                                                                                                            8 8 AMIDATION 852 MW; DC6365A5B9C8676A CRC64;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-2DPAGE; P31929; HUMAN.
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9 AA; 1129 MW;
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SEQUENCE, AND SYNTHESIS.
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Matches 2; Conserv
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Matches 3; Conserv
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1 DPGF 4
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P31929;
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TMOF_SARBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trimery Structures of hypertrehalosaemic neuropeptides isolated from acaded G., Rinehart K.L.

"Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardidates of the cockroaches Leucophaea maderae, acompladorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardement mass spectrometry.";

Biol. Chem. Hoppe-Seyler 371.345.354(1990).

-!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT ELEVALE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

-!- SIMILARRIY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

PIR: 508996.

RP PIR: 508996.

RP PIR: 508996.

RP PIR: 8498023; 8498023.
                                                                                                                                                                                                          MEDLINE-84298179; PubMed=6591205;
Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
Miller C.A., Schooley D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90160053; PubMed-2576128; Gaede G., Kellner R.; "The metabolic neuropeptides of the corpus cardiacum from the potato beetle and the American cockroach are identical."; Peptides 10:1287-1289(1989).
                                                             Rinehart K.L. Jr.;
"Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
Biochem. Biophys. Res. Commun. 124:350-358(1984).
             MEDLINE-85046530; Pubmed-6548628;
Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 11).
LeUCCKININ II (L-II).
Leucophaea maderae (Madeira cockroach).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pletrygota; Neoptera: Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.
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Pred. No. 8.9e+04;
L; Mismatches 2; Indels
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86745771A9D1A736 CRC64;
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50.0%;
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8 AA; 1006 MW;
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SPECIES-P.AMERICANA;
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Best Local Similarity
Matches 3; Conserv
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P21141;
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LCK2_LEUMA
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
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                                                                          MEDLINE=94286417; PubMed=7912428;
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66.7%;
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              Planorbidae, Helisoma
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
                                                            TISSUE=KIDNEY;
                                                                                                                       trivolvis.";
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FAR4_PANRE
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AC P2542
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                                                                    "Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.";
Regul. Pept. 50:61-72(1994).
-!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR EPITHELIUM AFTER A BLOOD MEAL.
                                         Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                        .;
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Eur. J. Biochem. 250:727-734(1997).
-!- SINCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide: Multigene family.
SEQUENCE 7 AA; 782 MW; 672879CDCB476ACO CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab).
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Cacarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                        Score 13; DB 1; Length 6; Pred. No. 8.9e+04; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                             6 AA; 695 MW; 61E72451B7642000 CRC64;
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30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE GDPFLRF-AMIDE.
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                            MEDLINE-94211930; PubMed-8159807;
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66.7%;
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AND SYNTHESIS
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                    DEVELOPMENT
            TISSUE=OVARY
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P81807;
                                                          de Loof A.;
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P41871;
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1 NPT 3
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FAR1_HELTI
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Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.; "FWRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95232026; PubMed=7716079; MEDLINE=95232026; PubMed=7716079; Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P., Thim L., Kubiak T.M., Martin R.A., Geary T.G.; "Isolation and preliminary biological characterization of KPNFIRFamide, a novel FMRFamide-related peptide from the free-living nematode, Panagrellus redivivus."; Peptides 16:87-93(1955).
--- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDIVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                      Peptides 15:31-36(1994).

-!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
-!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
-!- THE KIDNEY, MANTLE AND THE HEMOLYMPH.
-!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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Pred. No. 8.9e+04;
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Panagrolaimoidea, Panagrolaimidae, Panagrellus.
                                                                                                                                                                                                                                                                                                                                                                  7 AA; 851 MW; 69D40729D76AA810 CRC64;
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7 AA; 921 MW; 69D40059C4576350 CRC64;
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01-NoV-1995 (Rel. 32, Last sequence update)
01-NAX-2000 (Rel. 39, Last annotation update)
FMRFANIDE-LIKE NEUROPEPTIDE PF4 (KPNFIRFAMIDE)
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01-FEB-1994 (Rel. 28, Last sequence update)
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Conservative
                                                                                                                                            STANDARD;
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          Query Match
Best Local Similarity
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                                                                2 PTFKEN 7
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P04548;
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                                                                                                                                                                                                                            cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass beetrometry.";

Balol, Chem. Hoppe-Seyler 373:133-142(1992).

C. !- FUNCTION: THIS HORMONE, RELEASED FROM CELLS. IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGITICERIDES FROM THE FAT BOY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGITICENTES TO USE THESE DIGITICES AS AN ENERGY SOURCE.

1- SIMILARITY: BELONGS TO THE ARH / HRTH / RPCH FAMILY.

PIR; $15422.

INTERPRO TRANSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                         "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."; Blochem. J. 278:671-677(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Serum antibody responses of cats to soluble whole cell antigens of feline porphyromonas gingivalis.", Vet. Microbiol. 73:37-49(2000).
                                                                                                          SPECIES-M.MELOLONTHA, AND G.STERCOROSUS; TISSUE-CORPORA CARDIACA; MEDLINE-91248100; PubMed-2039445;
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Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
"Primary structures of neuropeptides isolated from the corpora
                              Geotrupes stercorosus (Dor beetle), and
Pachnoda marginata (Flower beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8;
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Bacteria, CFB group, Bacteroidaceae, Porphyromonas.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
44 KDA IMMUNOGENIC PROTEIN (FRAGMENT)
                                                                                                                                                                                                             SPECIES=P.MARGINATA; TISSUE=CORPORA CARDIACA;
 Last annotation update)
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Pred. No.
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          ADIPOKINETIC HORMONE (AKH).
Melolontha melolontha (Cockchafer),
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TRAIN-WEB 3492;
MEDLINE-20198497; PubMed-10731616;
Norris J.M., Love D.N.;
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Neuropeptide; Amidation; Flight.
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100.0%;
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MEDLINE-84298179; Pubmed-6591205;
Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
Miller C.A., Schooley D.A.;
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"Primary structures of hypertrehalosaemic neuropeptides isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-L.DECEMLINEATA; TISSUE-CORPORA CARDIACA;
MEDLINE-90160053; PubMed-2576128;
Gaede G., Kellner R.;
"The metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
Peptides 10:1287-1289(1989).
                                                                                                                      Gaps
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
02-FEB-1994 (Rel. 28, Last annotation update)
03-FEB-1994 (Rel. 28, Last annotation update)
04-FEB-1994 (Rel. 28, Last annotation u
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Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
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Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
                Length
     Score 13; DB 1; I
Pred. No. 8.9e+04;
0; Mismatches 3;
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25.0%;
50.0%;
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DR PROSITE; PS00256; AKH; 1.

KW Neuropeptide: Amidation.
FT MOD_RES 1 1 AMIDATION.
FT MOD_RES 8 AA; 991 MW; 8674577589C452D6 CRC64;

Query Match 25.0%; Score 13; DB 1; Length 8; Best Local Similarity 40.0%; Pred. No. 8.9e+04; Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps

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Qy 4 FKENY 8

Db 4 FSPNW 8

Search completed: January 17, 2001, 13:47:10 Job time: 279 sec

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Romaniec M.P., Fauth U., Kobayashi T., Huskisson N.S., Barker P.J.,
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2000 (TrEMBLrel. 14, Last annotation update)
1,4-BETA-D-GLUCAN GLUCANOHYDROLASE (EC 3.2.1.4) (FRAGMENT).
Clostridium thermocellum.
Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                 Demain A.L.;
Demain A.L.;
Purification and characterization of a new endoglucanase from Clostridium thermocellum.";
Biochem. J. 283:69-73(1992).
SEQUENCE 8 AA; 823 MW; C2C1ABIDD9D1B775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB 2; Length 8; Pred. No. 3.7e+05;
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01, Last sequence 08, Last anno
09R5R1
09P8E5
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031653
09TKG1
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80.0%;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
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NCBI_TaxID=1515;
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Ogr576 shigella dy
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Ogy4j3 homo sapien
Ogtke5 leptospermu
Q9wj33 peeudorabie
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Ogr779 heemophilus
Ogr779 chlamydia t
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Q9r7t2 escherichia
O98866 spinacia ol
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18.122 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                      January 17, 2001, 13:44:43
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Listing first 45 summaries
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Berne virus (BEV). Viruses; ssRNA positive-strand viruses, no DNA stage; Nidoviralus;

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                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lagoutte B., Vallon O.; Purification and membrane topology of PSI-D and PSI-E, two subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TREMBLrel. 13, Last annotation update)
PHOTOSYSTEM I REACTION CHTER SUBUNIT IV, PSI-E.
Spinacia oleracea (Spinach).
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OCBIQOPHYLLAID=3562;
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NCBI_TaxID=11120;
                                                                  is
                             SEQUENCE FROM N.A.
MEDLINE-90080137; PubMed=2293666;
Salider E.J., Horzinek M.C., Spaan W.J.M.;
Salider E.J., Horzinek M.C., Spaan W.J.M.;
A 3'-coterminal nested set of independently transcribed mRNAs generated during Berne virus replication.";
J. Virol. 64:331-338(1990).
EMBL: M33502; AAA42817.1;
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                                                                                                                      SEQUENCE 9 AA; 1234 MW; D8EE736B5451AB19 CRC64;
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Last annotation update)
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.. J. Biochem. 205:1175-1185(1992).
?UENCE 8 AA; 1082 MW; 2145BB1324069044 CRC64;
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1; Mismatches 0;
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avian infectious bronchitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92249324; PubMed=1374333;
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 Coronaviridae; Torovirus
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Best Local Similarity
Matches 3; Conserv
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Matches 3; Conserv
          NCBI_TaxID=11156;
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Santo N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
to the 12.7-28.0 min Region on the Linkage Map.";
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SEQUENCE FROM N.A.
MEDLINE-86120353; PubMed=3003688;
Sijben Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
"Spinach plastid genes coding for initiation factor IF-1, ribosomal
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NCBL_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Pred. No. 3.7e+05;
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Last annotation update)
(FRAGMENT).
                                                                             D2C4B33327741B46 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYTOCHROME B/F SUBUNIT IV (FRAGMENT).
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Pred. No. 3.7e+05;
0; Mismatches 1;
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J. Gen. Virol. 66:2253-2258(1985).
EMBL; M29338; AAA46234.1; -.
NON_TER
SEQUENCE 9 AA; 1134 MW; D2C4B3
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50.0%;
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75.0%;
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Chloroplast.
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Best Local Similarity 75.0
Matches 3; Conservative
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SEQUENCE FROM N.A.
TISSUE-FETAL LIYER;
MEDLINE-85155492; PubMed-6085063;
Urano Y., Sakai M., Watanabe K., Tamaoki T.;
"Tandem arrangement of the albumin and alpha-fetoprotein genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=FETAL LIVER;
MEDLINE=82081882; Pubmed=6171778;
Lawn R.M., Adelaman J., Bock S.C., Franke A.E., Houck C.M.,
Najarian R.C., Seeburg P.H., Wion K.L.;
"The sequence of human serum albumin cDNA and its expression in E.
                                                                                                                                                                                                                              ALB.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-FETAL LIVER;
MEDLINE-82105994; PubMed-6275391;
Dugatczyk A., Law S.W., Dennison O.E.;
"Nucleotide sequence and the encoded amino acids of human serum
Score 14; DB 11; Length 8;
Pred. No. 3.7e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.9%; Score 14; DB 4; Length 9; 50.0%; Pred. No. 3.7e+05; Live 1; Mismatches 1; Indels
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Gene 32:255-261(1984).
Gene 12:255-261(1984).
Gene 32:255-261(1984).
In 1 1 1 1 1 1 1 SEQUENCE 9 AA; 1186 MW; 92340B0400440681 CRC64;
                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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 26.9%;
66.7%;
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Kounnas M.Z., Wolz R.L., Gorbea C.M., Bond J.S.;
"Meptin-A and -B. Cell surface endopeptidases of the mouse kidney.";
J. Biol. Chem. 266:17350-17357(1991).
SEQUENCE. 8 AA: 877 MW; 43A5A76AB4069DD4 CRC64;
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MEDLINE-95002916; PubMed-7919324;
Tighe J.E., Calabi F.;
"Alternative, out-of-frame runt/MTG8 transcripts are encoded by the derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Washaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
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Q9Y4J4;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
RUNI/R2NI/MTGB PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blood 84:2115-2121(1994).
BMBL: S74092; AAD14144.1; -.
NON TER
SEQUENCE 8 AA: 1067 MW; 20F414044B17244B CRC64;
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Last annotation update)
                                                   NON_TER 1 1 SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;
protein S11 and RNA polymerase alpha-subunit.";
Nuclaic Acids Res. 14:1029-1044(1986).
BEBL: X03496; CAA27215.1; -.
Chloroplast.
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Best Local Similarity 75.0%;
Matches 3; Conservative (
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RAMAN MEDLINE-20196006; PubMed=10731132;

RAMAN MEDLINE-20196006; PubMed=10731132;

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RAMAN MED. Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RAMAN RAMAN MED. REAL E.G., Richards G., Champe M., Pfeiffer B.D.,

RAMAN K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RAMAN K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RAMAN R.H., Doyle C., Baxter E.G., Bandari D., Bolahakov S.,

RAMED R.M., Benos P.V., Bernan B.P., Bandari D., Bolahakov S.,

RAMAN Gawley S., Dahlke C., Davenpoort L., Beasley E.M.,

Burkis R.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,

RAMAN Cawley S., Dahlke C., Davenpoort L., Davies P.,

RAMAN Cawley S., Dahlke C., Davenpoort L., Davies P.,

RAMAN Cadielian A.E., Gary N.S., Gelbart W.M., Glasser R.,

RAMAN Cadielian A.E., Gary N.S., Gelbart W.M., Glasser R.,

RAMAN Cadielian A.E., Gary N.S., Gelbart W.M., Glasser R.,

RAMAN Cadelian A.E., Gary N.S., Gelbart W.M., Glasser R.,

RAMAN R.M., Houston R.A., Howland T.J., Hernandez J.R., Houck J.,

RAMEL B.E., Kodira C.D., Kraft C., Kraft C., Rennison J.A., Retchum R.A.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liux X., Mattei B., McIntosh T.C., McLeod M.P., McIson D.L.,

RAMING B.E., Kodira C.D., Kraft C., Rorleoler F., Smith T.,

Rayler E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Spier E., Spradling A.C., Pan S., Penlard J., Weissenbech J.,

RAMING B.E., Wassarman D.A., Weissenbech J.,

RAMING S.W., Woodes T., Woodes T., Weissenbech J.,

RAMING S.W., Woodes T., W
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
11,500 DA PRODUCT OF ORFA.
Shigella dysenteriae.
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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FLYBASE; FB9n0030380; CG18256.
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NCBI_TaxID=622;
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SEQUENCE.
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Polard P., Prere M.F., Chandler M., Fayet O.; "Programmed translational frameshifting and initiation at an AUU codon in gene expression of bacterial insertion sequence IS911."; Mol. Biol. 222:465-477(1991). SEQUENCE 8 AA: 935 MW; F4C5B9C45AB33336 CRC64;
                                                                                                                                                                                                                                        Gaps
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TISSUB-BONE MARROW;
MEDLINE-95002916; PubMed=7919324;
Tighe J.E., Calabi F.;
"Alternative, out-of-frame runt/MTG8 transcripts are encoded by the derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
RUNT/68NT/MTG8 PROTEIN (FRAGMENT).
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07, Last annotation update)
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                                                                                                                                                                                Score 13; DB 2; Pred. No. 3.7e+05;
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                                                                                                                                                     Query Match
Best Local Similarity 50.vv.,
-Local 2; Conservative
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Homo sapiens (Human).
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EMBL; L32078; AAA73888.1;
NON_TER 1
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SEQUENCE FROM N.A.
TISSUE-PLACENTA;
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
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SEQUENCE FROM N.A.
O'Brien M.M., Oulnn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0(2000).
EMBL; AF184690; AAF03860.1;
                                                                                       Gaps
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Chloroplast.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Myrtales; Myrtaceae; Leptospermum.
NCBI_TaxID=106049;
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                                                                                                                                                                                                                                                                                   Nicotiana palmeri, and Nicotiana bigelovii (Bigelov's tobacco)
                                                            Score 13; DB 4; Length 8;
Pred. No. 3.7e+05;
1; Mismatches 0; Indels
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Embl. 271234; CAA94933.1; -.
EMBL; 271225; CAA94921.1; -.
                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
RPS19'. PROTEIN (FRAGMENT).
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Last sequence update)
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EMBL; S74094; AAD14973.2; -.
NON_TER 1 1 SEQUENCE 8 AA; 929 MW; 30B764405B17244B CRC64;
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NON_TER 8 8 SEQUENCE 8 AA; 977 MW; FD43333735A411A6 CRC64;
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Best Local Similarity 40.0%; Pred. No. 3.7e+05;
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 4; Conservative
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Sequence 256, App
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(without alignments)
5.187 Million cell updates/sec
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Sequence 11,
Sequence 51,
Sequence 22,
Patent No. 549
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Sequence 4, R
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Sequence 5, R
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-US94-06654-4

US-08-325-553-5

US-08-394-152A-5

US-08-394-152A-5

US-08-310-912A-65

US-08-8110-912A-65

PCT-US95-04570-65

PCT-US95-04589-65

PCT-US95-0459-65

US-08-310-708-3

US-08-467-083-26

US-08-467-083-26

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US-08-467-4478-26

US-08-466-6808-26

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Listing first 45 summaries
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Match Length
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US-08-361-708-7

US-08-361-708-7

US-08-36-777-7

US-08-136-743B-66

US-08-136-743B-66

US-08-540-406-133

US-08-540-406-133

US-08-56-133

US-09-040-216-7

US-09-040-216-7

US-09-040-216-57

US-09-040-216-57

US-09-045-52-1323-13

US-08-125-258-69

US-08-7258-69

US-08-725-738-69

US-08-725-738-69

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US-08-725-738-69
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APPLICANT: Xian-feng Zhang, Ph.D.
TITLE OF INVENTION: INHIBITING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/Z MOdel 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark, Esq.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/190001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION UNBER:
FILING DATE: 19930611
CLASSIFICATION: 514
REIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/08077256
; Patent No. 5582995
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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Gaps
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US-08-460-533-4
; Sequence 4, Application US/08460533
; Patent No. 5767075
; GENERAL INFORMATION:
   APPLICANT: Joseph Avruch
   APPLICANT: Aian-Feng Zhang
   APPLICANT: Mark S. Marshall
   TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
   NUMBER OF SEQUENCES: 20
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Fish & Richardson P.C.
   STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 1;
Pred. No. 1.3e+05;
                                    COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READBLE FORM:
MEDIUW TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,351
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/259,672
FILING DATE: June 10, 1994
APPLICATION NUMBER: 08/077,256
FILING DATE: June 11, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark, ESq.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: US/08/460,533
FILING DATE: June 2, 1995
CLASSTRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NOTE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/259
FILING DATE: June 10, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 542-5070
TELES: 200154
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 50.۰۰
ممال مارید
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                       Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-459-351-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 F
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DPTFKENY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DPTIEDSY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.8%; Score 29; DB 1; Length 9; 50.0%; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Joseph Avruch
APPLICANT: Xian-Feng Zhang
APPLICANT: Mark S. Marshall
TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: TBM PS/2 Model 502 or 55xx
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/07/256
FILING DATE: June 11, 1993
ATTORNEY/AGENT INFORMATION:
NAME: PAUL T. Clark, ESG.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
RECISTRATION NUMBER: 30,162
RELECHNON: (617) 542-8906
TELEPHANE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                            APPLICANT: JOSEPH Avruch
APPLICANT: Xian-feng Zhang
APPLICANT: Mark S. Marshall
TITLE OF INVENTION: INHIBITING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C. STRGET: 225 Franklin Street
                                                                                                                                Sequence 4, Application US/08259672 Patent No. 5736337 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08459351
Patent No. 5763571
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.8
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                           STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 02110-2804
114 :::|
2 DPTIEDSY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DPTFKENY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                            US-08-259-672-4
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                  Score 29; DB 3; Length 9; Pred. No. 1.3e+05; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                          APPLICANT: Joseph Avruch
APPLICANT: Xian-feng Zhang
APPLICANT: Xian-feng Zhang
APPLICANT: Mark S. Marshall
TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: U.S.A.
2IP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55x
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06654
FILING DATE: Herewith
CLASSIPICATION:
                                                                                                                                                                                                RESULT 6
PCT-0594-06654-4
PCT-0594-06654-4
Sequence 4, Application PC/TUS9406654
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rademacher, Thomas W.
Manger, Ian D.
Wong, Simon
Dwek, Raymond A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence I, Application US/07926786
Patent No. 280113
GENERAL INFORMATION:
APPLICANT: Rademacher, Thomas W.
APPLICANT: Manger, Ian D.
APPLICANT: Wong, Simon APPLICANT: Dwek, Raymond A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Paul T. Clark, ESQ.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                    55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark, Eso
                                         Best_Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DPTIEDSY 9
                                                                                                  1 DPTFKENY 8
                                                                                                                           |||| :::|
2 DPTIEDSY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
TOPOLOGY:
PCT-US94-06654-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-926-786-1
                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                           55.8%; Score 29; DB 1; Length 9; 50.0%; Pred. No. 1.3e+05; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM COMPAtible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,836
FILING DATE: 11-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,274
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
              FILING DATE: June 11, 1993
ATTORNEY AGENT INFORMATION:
NAME: Paul T. Clark, Esq.
RECISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/234002
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Avruch, Joseph
APPLICANT: Luo, Zhujun
APPLICANT: Warshall, Mark S.
TITLE OF INVENTION: INHIBITING PROTEIN
ITLE OF INVENTION: INHIBITING PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00786/313001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Fish & Richardson, P.C. 225 Franklin Street
APPLICATION NUMBER: 08/077,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08814836
Patent No. 6103692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFRENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: No. 6103692e
US-08-814-836-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 9 amino acids amino acid
                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-460-533-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 225 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DPTIEDSY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DPTFKENY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-814-836-3
                                                                                                                                                                                                                                       LENGTH:
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US-08-394-152A-5
Sequence 5, Application US/08394152A
Sequence 5, Application US/08394152A
Sequence 5, Application US/08394152A
Sequence 5, Application S.
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 1; Length 7;
Pred. No. 1.38+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: ...
COUNTRY: United ...
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DXZ
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB 95
FILING ATTER: ATTER 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORING GENT TO NUMBER: US/07/973,337A
TOMBE: White, John P.
REGISTRATION NUMBER: 28,678
       APPLICATION NUMBER: US/08/325,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match Best Local Similarity 80.0"
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DPTFK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DPMFK 7
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US-08-325-553-5
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TITLE OF INVENTION: Method for Producing Synthetic N-Linked TITLE OF INVENTION: Glycoconjugates NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: SCOLT J. Meyer, Monsanto Co., A3SG STREET: 800 N. Lindbergh Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORNATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.2%; Score 24; DB 1; Length 5; 100.0%; Pred. No. 1.3e+05; Live 0; Mismatches 0; Indels
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-27(904)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America ZIP: 10112
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Patent No. 5538866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (314)694-3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-07-926-786-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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2 DPTF 5
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APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
CORRESPONDENCE: 208
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                   44.2%; Score 23; DB 2; Length 8; 80.0%; Pred. No. 1.3e+05; Live 1; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/310,912A FILING DATE: September 22, 1994
CLASSIFTCATION: 536
PROOR APPLICATION DATE: 894
APPLICATION NUMBER: 08/227,360
FILING DATE: APril 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/08310912A
Patent No. 5881730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M. APPLICANT: Staskawicz, Brian J. APPLICANT: Brent, Andrew F. APPLICANT: Dahlbeck, Douglas APPLICANT: Ratagiri, Fumiaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                       TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
COPCULE TYPE: peptide
US-08-669-2848-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
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Best Local Similarity 80.vv
-hes 4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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STRANDEDNESS: not
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COUNTRY: USA
ZIP: 02110-2904
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US-08-310-912A-65
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CITY: BC
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APPLICANT: Indoue, Makoto
APPLICANT: Isinge, Yoko
APPLICANT: Isinge, Yoko
APPLICANT: Ito, Akira
APPLICANT: Ito, Akira
APPLICANT: Kimura, Toru
APPLICANT: No. 5939534uchi, Hiroshi
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
NUMBER OF SEQUENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 2; Length 7; Pred. No. 1.3e+05; 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,284B
FILING DATE: 28-JUN-1996
PRIOR APPLICATION NUMBER: COT/JP94/02269
FILING DATE: 27-DEC-1994
PRIOR APPLICATION NUMBER: PT D6-268281
FILING DATE: OF-DCT-1994
PRIOR APPLICATION NUMBER: TO 6-268281
FILING DATE: OF-OCT-1994
PRIOR APPLICATION NUMBER: TO 6-268281
FILING DATE: OF-OCT-1994
PRIOR APPLICATION NUMBER: TO 6-268281
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                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEFICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-5
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FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-350934
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-669-284B-35; Sequence 35, Application US/08669284B; Patent No. 5939534
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REGIESTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: double
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44.2%; Score 23; DB 4; Length 8; 80.0%; Pred. No. 1.3e+05; live 0; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04570
                                                                                               APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kunkél, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
PCT-U595-04589-65
Sequence 65, Application PC/TUS9504589
GENERAL INFORMATION:
    Sequence 65, Application PC/TUS9504570
                                     Ausubel, Frederick M.
Staskawicz, Brian J.
Brent, Andrew F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ausubel, Frederick M.
Staskawicz, Brian J.
Brent, Andrew F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahlbeck, Douglas
Katagiri, Fumiaki
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amin 1
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Best Local Similarity 80.v.
A; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                              STATE:
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                  Score 23; DB 2; Length 8; Pred. No. 1.3e+05; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/841,089
                                                                                                                                                                                                                                                                                                               APPLICANT: Staskavicz, Brian J.
APPLICANT: Staskavicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Katagiri, Fumiaki
APPLICANT: Mindrinos, Michael N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
APPLICANT: Tu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILLING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DGORET NUMBER: 00786/230001
TELECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                         Sequence 65, Application US/08841089 Patent No. 6127607 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT: Ausubel, Frederick M.
                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                44.2%;
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TELEFAX: (617) 542-8906
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80.08;
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MEDIUM TYPE: Floppy disk
Ouery Match
Best Local Similarity 80.00
درم 4; Conservative
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TELEX: 100254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
44.2
Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-841-089-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110-2904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                   2 PTFKE 6
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3 PTFSE 7
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PCT-US95-04570-65
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US-08-841-089-65
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                                                                JDP-013DV
                 NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/COCKET NUMBER: JDP-
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                          35,965
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Query Match 42.3
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                             linear
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| TFEESFQ 7
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US-08-094-948A-21
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                                                                                  COUNTRY: USA
21P: 02110-2004

21P: 02110-2004

COMPUTER RADBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
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TELEPHONE: 617) 542-8070
TELEPHONE: 617) 542-8070
TELEPHONE: 617) 542-8070
TELEPHONE: 617) 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acids
TYPE: amino acids
TOWNING TINEAR
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,948A
FILING DATE: 21-JULY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08094948A
Fatent No. 5621075
GENERAL INFORMATION:
APPLICANT: Rahn, C. Ronald
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Bassachusetts
COUNTRY: U.S.A.
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-04589-65
               STREET: 225 E.
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3 PTFSE 7
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US-08-094-948A-21
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